DATE: Wednesday, October 29, 2003   Printable Copy   Create Case

Set Name side by side	**Query**	**Hit Count**	**Set Name** result set
DB=; PLUR=YES; OP=ADJ			
L6	'alpha d' same (antibod$) and (antibod$) same (inhibit$ or suppress$ or block$ or modulat$) same (tnf$ or tumor adj necrosis or tumour adj necrosis)	6	L6
L5	'alpha d' same (inhibit$ or suppress$ or block$ or modulat$) same (tnf$ or tumor adj necrosis or tumour adj necrosis)	12	L5
L4	'alpha d' and (tnf$ or tumor adj necrosis or tumour adj necrosis)	631	L4
L3	L1 and 'alpha d'	16	L3
DB=USPT,PGPB; PLUR=YES; OP=ADJ			
L2	L1 and alphad	1	L2
L1	gallatin.in.	73	L1

END OF SEARCH HISTORY

WEST

End of Result Set

Generate Collection   Print

L3: Entry 1 of 1   File: USPT   Jun 26, 2001

US-PAT-NO: 6251395
DOCUMENT-IDENTIFIER: US 6251395 B1
** See image for Certificate of Correction **

TITLE: Methods of inhibiting inflammation at the site of a central nervous system
injury with alphaD-specific antibodies

DATE-ISSUED: June 26, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Gallatin; W. Michael	Mercer Island	WA	98040	
Van der Vieren; Monica	Seattle	WA	98107	

US-CL-CURRENT: 424/144.1; 424/130.1, 424/141.1, 424/143.1, 424/153.1, 424/154.1,
424/173.1, 530/387.1, 530/388.1, 530/388.2, 530/388.22, 530/388.7, 530/388.73,
530/388.75

CLAIMS:

What is claimed is:

1. A method for inhibiting macrophage infiltration at the site of a central
nervous system injury comprising the step of administering to an individual an
effective amount of an anti-.alpha..sub.d monoclonal antibody.

2. The method according to claim 1 wherein the anti-.alpha..sub.d monoclonal
antibody blocks binding between .alpha..sub.d and a binding partner.

3. The method according to claim 2 wherein the binding partner is VCAM-1.

4. The method according to claim 1 where the anti-.alpha..sub.d monoclonal
antibody is selected from the group consisting of the monoclonal antibody secreted
by hybridoma 226H (ATCC Accession No: HB-12592) and the monoclonal antibody
secreted by hybridoma 236L (ATCC Accession No: HB-12593).

5. The method according to any one of claims 1 through 4 wherein the central
nervous system injury is a spinal cord injury.

6. A method for reducing inflammation at the site of a central nervous system
injury comprising the step of administering to an individual an effective amount
of an anti-.alpha..sub.d monoclonal antibody.

7. The method according to claim 6 wherein the anti-.alpha..sub.d monoclonal
antibody blocks binding between .alpha..sub.d and a binding partner.

8. The method according to claim 7 wherein the binding partner is VCAM-1.

9. The method according to claim 6 where the anti-.alpha..sub.d monoclonal
antibody is selected from the group consisting of the monoclonal antibody secreted
by hybridoma 226H (ATCC Accession No: HB-12592) and the monoclonal antibody
secreted by hybridoma 236L (ATCC Accession No: HB-12593).

WEST

⌐ Generate Collection ⌐ Print

L2: Entry 2 of 14   File: USPT   Aug 13, 2002

US-PAT-NO: 6432404
DOCUMENT-IDENTIFIER: US 6432404 B1

TITLE: Methods of inhibiting locomotor damage following spinal cord injury with
.alpha. D-specific antibodies

DATE-ISSUED: August 13, 2002

INVENTOR-INFORMATION:

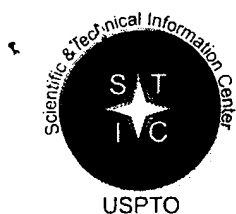| NAME	CITY	STATE	ZIP CODE	COUNTRY
Gallatin; W. Michael	Mercer Island	WA		
Van der Vieren; Monica	Snohomish	WA		

US-CL-CURRENT: 424/144.1; 424/130.1, 424/141.1, 424/143.1, 424/153.1, 424/154.1,
424/173.1, 530/387.1, 530/388.1, 530/388.2, 530/388.22, 530/388.7, 530/388.73,
530/388.75

CLAIMS:

What is claimed is:

1. A method for promoting locomotor recovery following spinal cord injury
comprising the step of administering to a spinal cord injury victim an effective
amount of an anti-.alpha..sub.d monoclonal antibody.

2. A method for inhibiting locomotor damage following spinal cord injury
comprising the step of administering to a spinal cord injury victim an effective
amount of an anti-.alpha..sub.d monoclonal antibody.

3. A method of limiting locomotor impairment following spinal cord injury
comprising the step of administering to a spinal cord injury victim an effective
amount of an anti-.alpha..sub.d monoclonal antibody.

4. A method of limiting autonomic and sensory dysfunction following spinal cord
injury comprising the step of administering to a spinal cord injury victim an
effective amount of an anti-.alpha..sub.d monoclonal antibody.

5. The method of any one of claims 1, 2, 3, or 4 wherein the anti-.alpha..sub.d
monoclonal antibody is secreted by a hybridoma selected from the group consisting
of 217L (ATCC Accession No: HB12701) and 226H (ATCC Accession No: 12502).

6. The method of any one of claims 1, 2, 3, or 4 wherein the anti-.alpha..sub.d
monoclonal antibody competes with 217L (ATCC Accession No: HB 12701) or 226H (ATCC
Accession No: 12502) for binding to .alpha..sub.d.

7. The method of any one of claims 1, 2, 3, or 4 wherein the anti-.alpha..sub.d
monoclonal antibody inhibits .alpha..sub.d binding to an .alpha..sub.d ligand.

8. The method according to any one of claims 1, 2, 3, or 4 wherein the spinal cord
injury comprises compression to the spinal cord.

9. The method of claim 7 wherein the .alpha..sub.d ligand is selected from the
group consisting of ICAM-R and VCAM-1.

10. The method according to any one of claims 6 through 9 wherein the central nervous system injury is a spinal cord injury.

STIC Search Report
Biotech-Chem Library

USPTO

TO: Phillip Gambel
Location: 8b03 / 9e12
Friday, August 29, 2003
Art Unit: 1644
Phone: 308-3997
Serial Number: 09 / 891943

From: Jan Delaval
Location: Biotech-Chem Library
CM1-1E07
Phone: 308-4498

jan.delaval@uspto.gov

Search Notes

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 – 703-308-4498
jan.delaval@uspto.gov

102298

From:	Gambel, Phillip
Sent:	Tuesday, August 26, 2003 9:26 AM
To:	Delaval, Jan
Subj ct:	09 / 891,943 ifw amd

jan

please perform a sequence and a sequence interference search for

ussn 09 / 891,943   (ifw amd)

SEQ ID NO: 1

SEQ ID NO: 2

thanx

phillip gambel
art unit 1644
308-3997

1644 mailbox 9e12

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 – 703-308-4498
ian.delaval@uspto.gov

1

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name _____ _____   Examiner # _____   Date _____
Art Unit _____   Phone Number 30_____   Serial Number _____
Mail Box and Bldg Room Location _____   Results Format Preferred (circle):   PAPER   DISK   E-MAIL

If more than one search is submitted, please prioritize searches in order of need.
****

Please provide a detailed statement of the search topic and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of invention: _____   _____   _____   _____

Inventors (please provide full names): _____ _____ _____ ___ __ _____

_____ ___ ____ _____ _____ _____ _____ ___ _____

Earliest Priority Filing Date _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number

.5

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 – 703-308-4498
jan.delaval@uspto.gov

....

STAFF USE ONLY

Searcher _____ (ar)	**Type of Search**	**Vendors and cost where applicable**
Searcher Phone # _____ 4458	NA Sequence (#) ___ ✓	STN _____
Search Location _____	AA Sequence (#) ___ ✓	Dialog _____
Date Searched _____ 8/26/03	Structure (# _____	Questel/Orbit _____
Date Completed _____ 8/28/03	Bibliographic _____	STN _____
Searcher Prep & Review Time _____	Litigation _____	Lexis/Nexis _____
Online Prep Time _____ 15	Full-text _____	Sequence Systems ✓ _____
Online Time _____ +15	Patent Family _____	Gene/Internet _____
Comments _____	Other _____	Sequence _____

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: August 28, 2003, 16:16:12 ; Search time 17399 Seconds
(without alignments)
8760.806 Million cell updates/sec

Title: US-09-891-943-1
Perfect score: 3726
Sequence: 1 tgacctcgcactgtgctt..........agcataaatttcatatgct 3726

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 2888711 seqs, 2045481336 residues
Total number of hits satisfying chosen parameters: 5777422
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: gb_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_vi:*
31: em_htg_hum:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3726	100.0	3726	6	AR044695	AR044695 Sequence
2	3726	100.0	3726	6	AR052342	AR052342 Sequence
3	3726	100.0	3726	6	AR055140	AR055140 Sequence
4	3726	100.0	3726	6	AR158011	AR158011 Sequence
5	3726	100.0	3726	6	AR222661	AR222661 Sequence
6	3726	100.0	3726	6	AX448965	AX448965 Sequence
7	3726	100.0	3726	6	BD070942	BD070942 Novel hum
8	3726	100.0	3726	6	I13528	I13528 Sequence 1
9	3726	100.0	3726	6	I15787	I15787 Sequence 1
10	3726	100.0	3726	6	I92491	I92491 Sequence 1
11	3699	99.3	3785	6	AR044775	AR044775 Sequence
12	3699	99.3	3785	6	AR052422	AR052422 Sequence
13	3699	99.3	3785	6	AR055220	AR055220 Sequence
14	3699	99.3	3785	6	AR158091	AR158091 Sequence
15	3699	99.3	3785	6	AR222741	AR222741 Sequence
16	3699	99.3	3785	6	AX449062	AX449062 Sequence
17	3699	99.3	3785	6	BD071022	BD071022 Novel hum
18	3699	99.3	3785	6	I92571	I92571 Sequence 98
19	3583	96.2	3956	6	AR044774	AR044774 Sequence
20	3583	96.2	3956	6	AR052421	AR052421 Sequence
21	3583	96.2	3956	6	AR055219	AR055219 Sequence
22	3583	96.2	3956	6	AR158090	AR158090 Sequence
23	3583	96.2	3956	6	AR222740	AR222740 Sequence
24	3583	96.2	3956	6	AX449061	AX449061 Sequence
25	3583	96.2	3956	6	BD071021	BD071021 Novel hum
26	3583	96.2	3956	9	I92570	I92570 Sequence 97
27	3484.6	93.5	3486	9	HSU37028	U37028 Human leuko
28	2315.2	62.1	3803	6	AR044732	AR044732 Sequence
29	2315.2	62.1	3803	6	AR052379	AR052379 Sequence
30	2315.2	62.1	3803	6	AR055177	AR055177 Sequence
31	2315.2	62.1	3803	6	AR158048	AR158048 Sequence
32	2315.2	62.1	3803	6	AR222698	AR222698 Sequence
33	2315.2	62.1	3803	6	AX449016	AX449016 Sequence
34	2315.2	62.1	3803	6	BD070979	BD070979 Novel hum
35	2315.2	62.1	3803	10	I92528	I92528 Sequence 52
36	2304.6	61.9	3558	6	AF021334	AF021334 Rattus no
37	2304.2	61.8	3597	6	AR044733	AR044733 Sequence
38	2304.2	61.8	3597	6	AR052380	AR052380 Sequence
39	2304.2	61.8	3597	6	AR055178	AR055178 Sequence
40	2304.2	61.8	3597	6	AR158049	AR158049 Sequence
41	2304.2	61.8	3597	6	AR222699	AR222699 Sequence
42	2304.2	61.8	3597	6	AX449018	AX449018 Sequence
43	2304.2	61.8	3597	6	BD070980	BD070980 Novel hum
44	2304.2	61.8	3597	6	I92529	I92529 Sequence 54
45	2300.2	61.7	3528	6	AR044718	AR044718 Sequence

RESULT 1
AR044695

```
LOCUS       AR044695                3726 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1 from patent US 5817515.
ACCESSION   AR044695
VERSION     AR044695.1  GI:5966160
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3726)
  AUTHORS   Gallatin,W.Michael. and Van der Vieren,M.
  TITLE     Human B2 integrin alpha subunit antibodies
  JOURNAL   Patent: US 5817515-A 1 06-OCT-1998;
FEATURES             Location/Qualifiers
```

ALIGNMENTS

BASE COUNT   817 a   1064 c   1054 g   791 t

source   1..3726
       /organism="unknown"

ORIGIN

Query Match   100.0%;   Score 3726;   DB 6;   Length 3726;
Best Local Similarity   100.0%;   Pred. No. 0;
Matches 3726;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

```
Qy      1 TGACCTTCCGCCACTGTGCTTCTTCCTTCCTTCTTTATCATCATCATCATCATCAACCTGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TGACCTTCCGCCACTGTGCTTCTTCCTTCCTTCTTTATCATCATCATCAACCTGG 60

Qy     61 ATGTGGAGGAGGCCTAGGATACTTCCAGGAGGGATGCAGGGGGCTTTGGGCCACAGGCGTGGTGC 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ATGTGGAGGAGGCCTACGAGATCTTCCAGGAGGGATGCAGGGGCCGGCTTGGGCCACAGCGTGGTGC 120
```

(sequence alignment continues, Qy/Db pairs through position 2100)

OM nucleic - nucleic search, using sw model

Copyright (c) 1993 - 2003 Compugen Ltd.

GenCore version 5.1.6

Run on: August 28, 2003, 16:12:37 ; Search time 1136 Seconds
(without alignments)
8853.967 Million cell updates/sec

Title: US-09-891-943-1
Perfect score: 3726
Sequence: 1 tgacctcggcactgtgctt..........agcataaatttcatatgct 3726

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
```
N Geneseq_19Jun03:*
 1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
 2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
 3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
 4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
 5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
 6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
 7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
 8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
 9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3726	100.0	3726	16	AAQ91712	Human beta 2 integ
2	3726	100.0	3726	18	AAT79220	Human beta 2 integ
3	3726	100.0	3726	19	AAV67281	Human alpha-d enco
4	3726	100.0	3726	19	AAV35236	Human beta-integri
5	3726	100.0	3726	19	AAV31540	Human beta2 integr
6	3726	100.0	3726	20	AAV08453	Human alphad codin
7	3726	100.0	3726	21	AAA60014	Human alpha_d clon
8	3726	100.0	3726	24	ABK82404	Human cDNA encodin

ALIGNMENTS

9	3699	99.3	3785	18	AAT79275	Human beta 2 integ
10	3699	99.3	3785	19	AAV67299	Human alpha-d deri
11	3699	99.3	3785	19	AAV35316	Human Beta-integri
12	3699	99.3	3785	20	AAV08458	Human alphad codin
13	3699	99.3	3785	21	AAA60094	Human alpha_d codi
14	3699	99.3	3785	24	ABK82484	Human Beta2 integr
15	3583	96.2	3956	18	AAT79274	Human beta 2 integ
16	3583	96.2	3956	19	AAV67298	Human alpha-d clon
17	3583	96.2	3956	19	AAV35315	Human Beta-integri
18	3583	96.2	3956	20	AAV08457	Human alphad codin
19	3583	96.2	3956	21	AAA60093	Human alpha_d clon
20	3583	96.2	3956	24	ABK82483	Human Beta2 integr
21	2315.2	62.1	3803	18	AAT79256	Mouse beta 2 integ
22	2315.2	62.1	3803	19	AAA60051	Mouse alpha-d enco
23	2315.2	62.1	3803	19	AAV35273	Mouse beta-integri
24	2315.2	62.1	3803	19	AAV31575	Mouse alpha-d poly
25	2315.2	62.1	3803	20	AAV08516	Mouse alphad codin
26	2315.2	62.1	3803	19	AAA60051	Mouse alpha_d codi
27	2315.2	62.1	3803	24	ABK82441	Mouse cDNA encodin
28	2313.6	62.1	3803	16	AAQ91714	Mouse alpha-d subu
29	2304.2	61.8	3597	16	AAT79257	Rat beta 2 integri
30	2304.2	61.8	3597	19	AAV67280	Rat alpha-d encodi
31	2304.2	61.8	3597	19	AAV35274	Rat beta-integrin
32	2304.2	61.8	3597	19	AAV31576	Rat alpha_d polype
33	2304.2	61.8	3597	20	AAV08476	Rat alphad coding
34	2304.2	61.8	3597	21	AAA60052	Rat alpha_d coding
35	2304.2	61.8	3597	24	ABK82442	Rat cDNA encoding
36	2302.6	61.8	3597	16	AAQ91715	Rat alpha-d subuni
37	2300.2	61.7	3528	16	AAQ91740	Rat alpha-d compos
38	2300.2	61.7	3528	18	AAT79243	Rat beta 2 integri
39	2300.2	61.7	3528	19	AAV63807	Rat alpha-d encodi
40	2300.2	61.7	3528	19	AAV31563	Rat alpha d polype
41	2300.2	61.7	3528	20	AAV08471	Rat alphad coding
42	2300.2	61.7	3528	21	AAA60037	Rat alpha_d partia
43	2300.2	61.7	3528	24	ABK82427	Rat cDNA encoding
44	2289	61.4	3526	19	AAV35259	Rat beta-integrin
45	2210.8	59.3	3519	16	AAQ91713	Mouse alpha-d subu

RESULT 1
AAQ91712

ID   AAQ91712 standard; cDNA; 3726 BP.
XX
AC   AAQ91712;
XX
DT   28-DEC-1995 (first entry)
XX
DE   Human beta-2 integrin alpha-d cDNA.
XX
KW   Beta-2 integrin alpha-d subunit; antiinflammatory; arteriosclerosis;
KW   inflammatory bowel disease; asthma; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FH
FT   CDS   3..3488
FT   /*tag= a
XX
PN   WO9517412-A1.
XX
PD   29-JUN-1995.
XX
PF   21-DEC-1994; 94WO-US14832.
XX
PR   05-AUG-1994; 94US-0286889.
PR   23-DEC-1993; 93US-0173497.
XX
PA   (ICOS-) ICOS CORP.
XX
PI   Gallatin WM, Van Der Vieren M;

```
XX
DR   WPI; 1995-240603/31.
DR   P-PSDB; AAR78166.
XX
PT   Alpha sub-unit polypeptide of human beta 2 integrin - used to
PT   identify potential antiinflammatory agents, for the treatment of
PT   graft arteriosclerosis, inflammatory bowel disease, asthma, etc.
XX
PS   Claim 1; Page 82-87; 172pp; English.
XX
CC   A probe based on a partial cDNA clone (given in AAQ91727) of canine
CC   alpha-TM1 was used to screen a human spleen cDNA library to identify
CC   clone 19A2 encoding the beta-1 integrin alpha-subunit, alpha-d.
CC   The cDNA was manipulated to allow expression of recombinant alpha-d
CC   subunit in COS and CHO cells.
XX
SQ   Sequence 3726 BP; 817 A; 1064 C; 1054 G; 791 T; 0 other;

  Query Match             100.0%;  Score 3726;  DB 16;  Length 3726;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 3726;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACCTTCGGCACTGTGCTTCTTCTGAGTGTCCTGGCTTCTTATCATGGATTCAACCTGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TGACCTTCGGCACTGTGCTTCTTCTGAGTGTCCTGGCTTCTTATCATGGATTCAACCTGG 60

Qy         61 ATGTGGAGGAGCCTACGATCTTCCAGGAGGATGCAGGCGGCTTTGGGCAGAGCGTGGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGTGGAGGAGCCTACGATCTTCCAGGAGGATGCAGGCGGCTTTGGGCAGAGCGTGGTGC 120

Qy        121 AGTTCGGTGGATCTCGACTCGTGGTGGGAGCACCCCTGGAGGTGGTGGCGGCCAACCAGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGTTCGGTGGATCTCGACTCGTGGTGGGAGCACCCCTGGAGGTGGTGGCGGCCAACCAGA 180

Qy        181 CGGGACGGCTGTATGACTGCGCAGCTGCCACCGGCATGTGCCAGCCCATCCCGCTGCACA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGGGACGGCTGTATGACTGCGCAGCTGCCACCGGCATGTGCCAGCCCATCCCGCTGCACA 240

Qy        241 TCCGCCCTGAGGCCGTGAACATGTCCTTGGGCCTGACCCTGGCAGCCTCCACCAACGGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCGCCCTGAGGCCGTGAACATGTCCTTGGGCCTGACCCTGGCAGCCTCCACCAACGGCT 300

Qy        301 CCCGGCTCCTGGCCTGTGGCCCGACCCTGCACAGAGTCTGTGGGGAGAACTCATACTCAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCCGGCTCCTGGCCTGTGGCCCGACCCTGCACAGAGTCTGTGGGGAGAACTCATACTCAA 360

Qy        361 AGGGTTCCTGCCTCCTGCTGGGCTCGCGCTGGGAGATCATCCAGACAGTCCCCGACGCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGGGTTCCTGCCTCCTGCTGGGCTCGCGCTGGGAGATCATCCAGACAGTCCCCGACGCCA 420

Qy        421 CGCCAGAGTGTCCACATCAAGAGATGGACATCGTCTTCCTGATTGACGGCTCTGGAAGCA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CGCCAGAGTGTCCACATCAAGAGATGGACATCGTCTTCCTGATTGACGGCTCTGGAAGCA 480

Qy        481 TTGACCAAAATGACTTTAACCAGATGAAGGGCTTTGTCCAAGCTGTCATGGGCCAGTTTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTGACCAAAATGACTTTAACCAGATGAAGGGCTTTGTCCAAGCTGTCATGGGCCAGTTTG 540

Qy        541 AGGGCACTGACACCCTGTTTGCACTGATGCAGTACTCAAACCTCCTGAAGATCCACTTCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGGGCACTGACACCCTGTTTGCACTGATGCAGTACTCAAACCTCCTGAAGATCCACTTCA 600

Qy        601 CCTTCACCCAATTCCGGACCAGCCCGAGCCAGCAGAGCCTGGTGGATCCCATCGTCCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCTTCACCCAATTCCGGACCAGCCCGAGCCAGCAGAGCCTGGTGGATCCCATCGTCCAAC 660

Qy        661 TGAAAGGCCTGACGTTCACGGCCACGGGCATCCTGACAGTGGTGACACAGCTATTTCATC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGAAAGGCCTGACGTTCACGGCCACGGGCATCCTGACAGTGGTGACACAGCTATTTCATC 720

Qy        721 ATAAGAATGGGGCCCGAAAAAGTGCCAAGAAGATCCTCATTGTCATCACAGATGGGCAGA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATAAGAATGGGGCCCGAAAAAGTGCCAAGAAGATCCTCATTGTCATCACAGATGGGCAGA 780

Qy        781 AGTACAAAGACCCCCTGGAATACAGTGATGTCATCCCCCAGGCAGAGAAGGCTGGCATCA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AGTACAAAGACCCCCTGGAATACAGTGATGTCATCCCCCAGGCAGAGAAGGCTGGCATCA 840

Qy        841 TCCGCTACGCTATCGGGGTGGGACACGCTTTCCAGGGACCCACTGCCAGGCAGGAGCTGA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCCGCTACGCTATCGGGGTGGGACACGCTTTCCAGGGACCCACTGCCAGGCAGGAGCTGA 900

Qy        901 ATACCATCAGCTCAGCGCCTCCGCAGGACCACGTGTTCAAGGTGGACAACTTTGCAGCCC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATACCATCAGCTCAGCGCCTCCGCAGGACCACGTGTTCAAGGTGGACAACTTTGCAGCCC 960

Qy        961 TTGGCAGCATCCAGAAGCAGCTGCAGGAGAAGATCTATGCAGTTGAGGGAACCCAGTCCA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGGCAGCATCCAGAAGCAGCTGCAGGAGAAGATCTATGCAGTTGAGGGAACCCAGTCCA 1020

Qy       1021 GGGCAAGCAGCTCCTTCCAGCACGAGATGTCCCAAGAAGGCTTCAGCACAGCCCTCACAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGGCAAGCAGCTCCTTCCAGCACGAGATGTCCCAAGAAGGCTTCAGCACAGCCCTCACAA 1080

Qy       1081 TGGATGGCCTCTTCCTGGGGGCTGTGGGGAGCTTTAGCTGGTCTGGAGGTGCCTTCCTGT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGGATGGCCTCTTCCTGGGGGCTGTGGGGAGCTTTAGCTGGTCTGGAGGTGCCTTCCTGT 1140

Qy       1141 ATCCCCCAAATATGAGCCCCACCTTCATCAACATGTCTCAGGAGAATGTGGACATGAGGG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATCCCCCAAATATGAGCCCCACCTTCATCAACATGTCTCAGGAGAATGTGGACATGAGGG 1200

Qy       1201 ACTCTTACCTGGGTTACTCCACCGAGCTAGCCCTGTGGAAGGGGGTACAGAACCTGGTCC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 ACTCTTACCTGGGTTACTCCACCGAGCTAGCCCTGTGGAAGGGGGTACAGAACCTGGTCC 1260

Qy       1261 TGGGGGCCCCCCGCTACCAGCATACCGGGAAGGCTGTCATCTTCACCCAGGTGTCCAGGC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TGGGGGCCCCCCGCTACCAGCATACCGGGAAGGCTGTCATCTTCACCCAGGTGTCCAGGC 1320

Qy       1321 AATGGAGGAAGAAGGCCGAAGTCACAGGGACGCAGATCGGCTCCTACTTCGGGGCCTCCC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AATGGAGGAAGAAGGCCGAAGTCACAGGGACGCAGATCGGCTCCTACTTCGGGGCCTCCC 1380

Qy       1381 TCTGCTCCGTGGATGTGGACAGCGATGGCAGCACCGACCTGATCCTCATTGGGGCCCCCC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TCTGCTCCGTGGATGTGGACAGCGATGGCAGCACCGACCTGATCCTCATTGGGGCCCCCC 1440

Qy       1441 ATTACTATGAGCAGACCCGAGGGGGCCAGGTGTCCGTGTGTCCCTTGCCTAGGGGGCAGA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 ATTACTATGAGCAGACCCGAGGGGGCCAGGTGTCCGTGTGTCCCTTGCCTAGGGGGCAGA 1500

Qy       1501 GGGTGCAGTGGCAGTGTGACGCTGTTCTCCGTGGTGAGCAGGGCCACCCCTGGGGCCGCT 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GGGTGCAGTGGCAGTGTGACGCTGTTCTCCGTGGTGAGCAGGGCCACCCCTGGGGCCGCT 1560

Qy       1561 TTGGGGCAGCCCTGACAGTGTTGGGGGATGTGAATGAGGACAAGCTGATAGACGTGGCCA 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TTGGGGCAGCCCTGACAGTGTTGGGGGATGTGAATGAGGACAAGCTGATAGACGTGGCCA 1620

Qy       1621 TTGGGGCCCCGGGAGAGCAGGAGAACCGGGGTGCTGTCTACCTGTTTCACGGAGCCTCAG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 TTGGGGCCCCGGGAGAGCAGGAGAACCGGGGTGCTGTCTACCTGTTTCACGGAGCCTCAG 1680

Qy       1681 AATCCGGCATCAGCCCCTCCCACAGCCAGCGGATTGCCAGCTCCCAGCTCTCCCCCAGGC 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 AATCCGGCATCAGCCCCTCCCACAGCCAGCGGATTGCCAGCTCCCAGCTCTCCCCCAGGC 1740

Qy       1741 TGCAGTATTTTGGGCAGGCGCTGAGTGGGGGTCAGGACCTCACCCAGGATGGACTGATGG 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 TGCAGTATTTTGGGCAGGCGCTGAGTGGGGGTCAGGACCTCACCCAGGATGGACTGATGG 1800

Qy       1801 ACCTGGCCGTGGGGGCCCGGGGCCAGGTGCTCCTGCTCAGGAGTCTGCCGGTGCTGAAAG 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 ACCTGGCCGTGGGGGCCCGGGGCCAGGTGCTCCTGCTCAGGAGTCTGCCGGTGCTGAAAG 1860
```

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: August 29, 2003, 00:24:39 ; Search time 1836 Seconds
                    (without alignments)
                    4655.980 Million cell updates/sec

Title: US-09-891-943-1
Perfect score: 3726
Sequence: 1 tgaccttcggcactgtgctt..........agcataaattcatatgct 3726

Scoring table: IDENTITY_NUC
                    Gapop 10.0 , Gapext 1.0

Searched: 1533700 seqs, 1147125425 residues

Total number of hits satisfying chosen parameters: 3067400

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications NA.*
        1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
        2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
        3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
        4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
        5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
        6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
        7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
        8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
        9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
       10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
       11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
       12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
       13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
       14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
       15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
       16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
       17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3726	100.0	3726	9	US-09-350-259-1	Sequence 1, Appli
2	3726	100.0	3726	11	US-09-891-943-1	Sequence 1, Appl
3	3699	99.3	3785	9	US-09-350-259-98	Sequence 98, Appl
4	3699	99.3	3785	11	US-09-891-943-98	Sequence 98, Appl
5	3583	96.2	3956	9	US-09-350-259-97	Sequence 97, Appl
6	3583	96.2	3956	11	US-09-891-943-97	Sequence 97, Appl
7	2315	62.1	3803	9	US-09-350-259-52	Sequence 52, Appl
8	2315.2	62.1	3803	11	US-09-891-943-52	Sequence 52, Appl
9	2304.2	61.8	3597	9	US-09-350-259-54	Sequence 54, Appl
10	2304.2	61.8	3597	11	US-09-891-943-54	Sequence 54, Appl
11	2300.2	61.7	3528	9	US-09-350-259-36	Sequence 36, Appl
12	2300.2	61.7	3528	11	US-09-891-943-36	Sequence 36, Appl
13	2210.8	59.3	3519	9	US-09-350-259-45	Sequence 45, Appl
14	2210.8	59.3	3519	11	US-09-891-943-45	Sequence 45, Appl
15	2138	57.4	2499	9	US-09-350-259-96	Sequence 96, Appl
16	2138	57.4	2499	11	US-09-891-943-96	Sequence 96, Appl
17	1628.8	43.7	4740	10	US-09-945-265-3	Sequence 3, Appli
18	1628.8	43.7	4740	11	US-09-902-481A-2	Sequence 2, Appli
19	1628.8	43.7	4740	14	US-10-207-655-175	Sequence 175, App
20	937	25.1	1484	9	US-09-891-943-102	Sequence 102, App
21	937	25.1	1484	11	US-09-350-259-102	Sequence 102, App
22	824.4	22.1	1318	9	US-09-350-259-100	Sequence 100, App
23	824.4	22.1	1318	11	US-09-891-943-100	Sequence 100, App
24	624.6	16.8	1006	9	US-09-350-259-24	Sequence 24, Appl
25	624.6	16.8	1006	11	US-09-891-943-24	Sequence 24, Appl
26	494.2	13.3	852	9	US-09-350-259-92	Sequence 92, Appl
27	494.2	13.3	852	11	US-09-891-943-92	Sequence 92, Appl
28	297.6	8.0	4045	9	US-09-805-517A-37	Sequence 37, Appl
29	280.2	7.5	597	14	US-10-066-557-12	Sequence 12, Appl
30	279.2	7.5	750	11	US-09-350-259-35	Sequence 35, Appl
31	275	7.4	481	11	US-10-102-806-35	Sequence 35, Appl
32	268.2	7.2	670	12	US-10-002-631C-196	Sequence 196, App
33	256.4	6.9	5133	10	US-09-945-265-1	Sequence 1, Appli
34	193.8	5.2	3927	12	US-10-177-55-1	Sequence 1, Appli
35	130.6	3.5	2125	9	US-10-125-540-48	Sequence 48, Appl
36	130.6	3.5	2125	14	US-09-984-130-25	Sequence 25, Appl
37	130.6	3.5	4631	11	US-09-836-353A-25	Sequence 25, Appl
38	130.6	3.5	4631	12	US-09-984-130-17	Sequence 17, Appl
39	130.6	3.5	4995	11	US-10-027-632-141582	Sequence 141582,
40	130.6	3.5	4995	12	US-10-027-632-141583	Sequence 141583,
41	115	3.1	501	13	US-10-027-632-141583	Sequence 141583,
42	115	3.1	501	13	US-09-866-050A-479	Sequence 479, App
43	67.8	1.8	2100	11	US-09-866-050A-479	Sequence 479, App
44	67.8	1.8	2100	14	US-10-152-661-479	Sequence 479, App
45	67.8	1.8	3380	11	US-09-866-050A-514	Sequence 514, App

ALIGNMENTS

RESULT 1
US-09-350-259-1

Sequence 1, Application US/09350259

Patent No. US20020062008A:
GENERAL INFORMATION:
  APPLICANT: Gallatin, Michael W.
  APPLICANT: Van der Vieren, Monica
  TITLE OF INVENTION: No. US20020062008Alel Human 2
  FILE REFERENCE: 27866/35004
  CURRENT APPLICATION NUMBER: US/09/350,259
  CURRENT FILING DATE: 1999-07-08
  EARLIER APPLICATION NUMBER: 09/193,043
  EARLIER APPLICATION NUMBER: 08/943,363
  EARLIER APPLICATION NUMBER: 08/173,497
  EARLIER FILING DATE: 1993-12-23
  EARLIER FILING DATE: 1997-10-03
  EARLIER FILING DATE: 1994-12-21
  EARLIER APPLICATION NUMBER: 08/362,652
  EARLIER FILING DATE: 1998-11-16
  EARLIER APPLICATION NUMBER: 09/193,043
  EARLIER FILING DATE: 1994-08-05
  EARLIER FILING DATE: 1993-12-23
  EARLIER APPLICATION NUMBER: 08/286,889
  NUMBER OF SEQ ID NOS: 114
  SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
  LENGTH: 3726
  TYPE: DNA
  ORGANISM: Homo sapiens
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (3)..(3485)
US-09-350-259-1

Query Match   100.0%; Score 3726; DB 9; Length 3726;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 3726; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 TGACCTTCGGCGACTGTGCTTCTTCTTCTGAGTGTCCTGGCTTCTTCTTATCATGGATTCAACCTGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 TGACCTTCGGCGACTGTGCTTCTTCTTCTGAGTGTCCTGGCTTCTTCTTATCATGGATTCAACCTGG 60

OM nucleic - nucleic search, using sw model

Copyright (c) 1993 - 2003 Compugen Ltd.
GenCore version 5.1.6

Run on: August 28, 2003, 19:08:18 ; Search time 308 seconds
(without alignments)
5339.589 Million cell updates/sec

Title: US-09-891-943-1
Perfect score: 3726
Sequence: 1 tgaccttcggcactgtgctt..........agcataaattttcatatgct 3726

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3726	100.0	3726	1	US-08-173-497-1	Sequence 1, Appl
2	3726	100.0	3726	1	US-08-286-889-1	Sequence 1, Appl
3	3726	100.0	3726	1	US-08-485-618-1	Sequence 1, Appl
4	3726	100.0	3726	1	US-08-362-652-1	Sequence 1, Appl
5	3726	100.0	3726	1	US-08-605-672-1	Sequence 1, Appl
6	3726	100.0	3726	1	US-08-482-293A-1	Sequence 1, Appl
7	3726	100.0	3726	2	US-08-943-363-1	Sequence 1, Appl
8	3726	100.0	3726	3	US-09-193-043-1	Sequence 1, Appl
9	3726	100.0	3726	4	US-09-688-307A-1	Sequence 1, Appl
10	3699	99.3	3785	1	US-08-485-618-98	Sequence 98, Appl
11	3699	99.3	3785	1	US-08-605-672-98	Sequence 98, Appl
12	3699	99.3	3785	2	US-08-482-293A-98	Sequence 98, Appl
13	3699	99.3	3785	2	US-08-943-363-98	Sequence 98, Appl
14	3699	99.3	3785	2	US-09-193-043-98	Sequence 98, Appl
15	3699	99.3	3785	4	US-09-688-307A-98	Sequence 98, Appl
16	3583	96.2	3956	1	US-08-485-618-97	Sequence 97, Appl
17	3583	96.2	3956	1	US-08-605-672-97	Sequence 97, Appl
18	3583	96.2	3956	2	US-08-482-293A-97	Sequence 97, Appl
19	3583	96.2	3956	2	US-08-943-363-97	Sequence 97, Appl
20	3583	96.2	3956	2	US-09-193-043-97	Sequence 97, Appl
21	3583	96.2	3956	4	US-09-688-307A-97	Sequence 97, Appl
22	2315.2	62.1	3803	1	US-08-485-618-52	Sequence 52, Appl
23	2315.2	62.1	3803	1	US-08-362-652-52	Sequence 52, Appl
24	2315.2	62.1	3803	2	US-08-605-672-52	Sequence 52, Appl
25	2315.2	62.1	3803	2	US-08-482-293A-52	Sequence 52, Appl
26	2315.2	62.1	3803	2	US-08-943-363-52	Sequence 52, Appl
27	2315.2	62.1	3803	3	US-09-193-043-52	Sequence 52, Appl
28	2315.2	62.1	3803	4	US-09-688-307A-52	Sequence 52, Appl
29	2304.2	61.8	3597	1	US-08-485-618-54	Sequence 54, Appl
30	2304.2	61.8	3597	1	US-08-362-652-54	Sequence 54, Appl
31	2304.2	61.8	3597	1	US-08-605-672-54	Sequence 54, Appl
32	2304.2	61.8	3597	2	US-08-482-293A-54	Sequence 54, Appl
33	2304.2	61.8	3597	2	US-08-943-363-54	Sequence 54, Appl
34	2304.2	61.8	3597	2	US-09-193-043-54	Sequence 54, Appl
35	2304.2	61.8	3597	4	US-09-688-307A-54	Sequence 54, Appl
36	2300.2	61.7	3528	1	US-08-286-889-36	Sequence 36, Appl
37	2300.2	61.7	3528	1	US-08-485-618-36	Sequence 36, Appl
38	2300.2	61.7	3528	1	US-08-362-652-36	Sequence 36, Appl
39	2300.2	61.7	3528	1	US-08-605-672-36	Sequence 36, Appl
40	2300.2	61.7	3528	2	US-08-482-293A-36	Sequence 36, Appl
41	2300.2	61.7	3528	2	US-08-943-363-36	Sequence 36, Appl
42	2300.2	61.7	3528	3	US-09-193-043-36	Sequence 36, Appl
43	2210.8	59.3	3519	1	US-09-688-307A-36	Sequence 36, Appl
44	2210.8	59.3	3519	1	US-08-286-889-45	Sequence 45, Appl
45	2210.8	59.3	3519	1	US-08-485-618-45	Sequence 45, Appl

ALIGNMENTS

RESULT 1
US-08-173-497-1
Sequence 1, Application US/08173497
Patent No. 5437958
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van Der Vieren, Monica
TITLE OF INVENTION: No. 5437958el Human 2 Integrin Alpha
TITLE OF INVENTION: Subunit
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 S. Wacker Drive, 6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,497
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No 5437958and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/31363
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3726 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 3..3485
US-08-173-497-1

Query Match   100.0%; Score 3726; DB 1; Length 3726;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 3726; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1   TGACCTTCGGCCACTGTTGCCTTCTTCTCTGAGTGTCCTGGGCTTCTTCTTTATCATGGATTCAACCTGG   60
Db   1   TGACCTTCGGCCACTGTTGCTTCTTCTTCTGAGTGTCCTGGGCTTCTTTATCATGGATTCAACCTGG   60

Qy   61   ATGTGGAGGAGGCTTACAGATCTTCCAGGAGGATGGCAGAGGCGGGCGGGTGGTGC   120
Db   61   ATGTGGAGGAGGCTTACAGATCTTCCAGGAGGATGGCAGAGGCGGGCGGGTGGTGC   120

Qy   121   AGTTCGGTGGATCGGACTCGTGCTGTGGGGAGCACCCCTGGAGGTTGGTGGCCAACCAGA   180

[DNA sequence alignment — query (Qy) versus database (Db) sequences, continuing in numbered blocks of 60 nucleotides per line through position ~2220]

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 26, 2003, 10:31:43 ; Search time 50 Seconds
(without alignments)
2233.037 Million cell updates/sec

Title: US-09-891-943-2
Perfect score: 5987
Sequence: 1 TFGTVLLLSVLASYHGFNLD..........DTATFSGDDFSCVAPNVPLS 1161

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR_76:*
2: pir1:*
3: pir2:*
4: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	3818	63.8	1163	1	RWHU1C	cell surface glyco
2	3455	57.7	1153	1	RWHU1B	cell surface glyco
3	3327.5	55.6	1153	1	RWHU1B	leukocyte surface
4	1474	24.6	1170	2	S00551	cell surface glyco
5	1457.5	24.3	1163	2	S00308	lymphocyte fuction
6	1148	19.2	1179	2	S56126	integrin alpha-E c
7	1030.5	17.2	1179	2	A53213	integrin alpha-1 c
8	1030.5	17.2	1180	2	A45226	integrin alpha-1 c
9	1012	16.9	1178	2	A35854	VLA-2 protein homo
10	1007.5	16.8	1180	2	S44142	integrin alpha 2 s
11	1007.5	16.8	1170	2	I45914	integrin alpha-2 c
12	1007.5	16.8	1181	2	A33998	integrin alpha-4 c
13	654.5	10.9	1038	2	S06046	lymphocyte-Peyer's
14	646.5	10.8	1034	2	A41131	alphaP integrin -
15	638	10.7	1054	2	JC7224	integrin alpha cha
16	611	10.2	1041	2	T31437	integrin alpha-9 c
17	584.5	9.8	1035	2	I58809	VLA-3 alpha subuni
18	579.5	9.7	1053	2	I55534	cell surface glyco
19	576.5	9.6	1051	2	A35761	glycoprotein IIb -
20	555	9.3	1037	2	A60163	fibronectin recept
21	552	9.2	1049	2	A27079	integrin alpha-2b
22	548	9.2	1039	2	A34269	integrin alpha-3 c
23	547.5	9.1	1051	2	A40021	integrin alpha-3 c
24	535.5	9.0	1053	2	S44250	integrin alpha-V c
25	534	8.9	1034	2	A36108	integrin alpha-V c
26	524.5	8.8	1034	2	A29937	position-specific
27	497	8.3	1044	2	T10050	integrin alpha-v c
28	496.5	8.3	1072	2	A38457	integrin alpha-6 c
29	493	8.2	1146	2	A27421	integrin alpha-5 c
29	492	8.2	1146	2	S40311	integrin - fruit f

30	477.5	8.0	1044	2	S16516	integrin alpha-8 c
31	473	7.9	1073	2	B36429	integrin alpha-6 c
32	464	7.8	1137	2	JC5950	integrin alpha-7 c
33	462.5	7.7	1091	2	A41543	integrin alpha-6 c
34	446.5	7.5	1045	2	S60571	integrin alpha v -
35	439	7.3	1135	2	161186	alpha-7 integrin -
36	433.5	7.2	1115	2	T09433	integrin alpha cha
37	431.5	7.2	1115	2	T09403	integrin alpha cha
38	431.5	7.2	1226	2	S44824	F54F2.1 protein -
39	420.5	7.0	1106	2	S38783	integrin alpha cha
40	410.5	6.9	764	2	I36916	glycoprotein IIb -
41	394	6.6	1139	2	S28277	hypothetical prote
42	322.5	5.4	272	2	A55548	integrin alpha-1 -
43	319.5	5.3	126	2	B30892	leukocyte adhesior
44	319.5	5.3	1086	2	T18523	integrin alpha cha
45	313.5	5.2	604	2	I36917	glycoprotein IIb -

ALIGNMENTS

RESULT 1
RWHU1C
cell surface glycoprotein CD11c precursor - human
N;Alternate names: leukocyte adhesion receptor p150,95 alpha chain
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text_change 22-Jun-1999
C;Accession: A36584; A35543; S00864
R;Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.
J. Biol. Chem. 265, 12750-12751, 1990
A;Reference number: A36584
A;Molecule type: DNA
A;Residues: 1-834 <CO2>
A;Contents: erratum
A;Accession: A36584
A;Molecule type: DNA
A;Residues: 1-1163 <COR>
A;Note: this revision to the sequence from reference A35543 includes the carboxyl end
R;Corbi, A.L.; Miller, L.J.; O'Connor, K.; Larson, R.S.; Springer, T.A.
EMBO J. 6, 4023-4028, 1987
A;Title: CDNA cloning and complete primary structure of the alpha subunit of a leuko
A;Reference number: S00864; A35543; MUID:88166645; PMID:3327687
A;Accession: S00864
A;Molecule type: mRNA
A;Residues: 1-755; 'L', 757-1163 <CO3>
A;Cross-references: GB:M81695; EMBL:Y00093; NID:g487829; PIDN:AAA59180.1; PID:g487830
A;Note: part of this sequence was confirmed by protein sequencing
R;Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.
J. Biol. Chem. 265, 2782-2788, 1990
A;Title: Genomic structure of an integrin alpha subunit, the leukocyte p150,95 molecu
A;Reference number: A35543; MUID:90153906; PMID:2303426
A;Accession: A35543
A;Molecule type: DNA
A;Residues: 1-834 <CO2>
A;Note: this sequence has been revised in reference A36584
C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat h
C;Keywords: calcium; cell adhesion; glycoprotein; heterodimer; magnesium; tandem repe
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1163/Product: cell surface glycoprotein CD11c #status predicted <MAT>
F;20-1107/Domain: extracellular #status prediced <EXT>
F;149-319/Domain: cell surface glycoprotein CD11c #status predicted <EXT>
F;1108-1133/Domain: von Willebrand factor type A repeat homology <VWA>
F;1134-1163/Domain: transmembrane #status predicted <TMM>
F;1134-1163/Domain: intracellular #status predicted <INT>
F;61,89,392,697,735,899,939,1050/Binding site: carbohydrate (Asn) (covalent) #status
A;Gene: GDB:ITGAX; CD11C
A;Cross-references: GDB:119758; OMIM:151510
A;Map position: 16p11.2-16p11.2
A;Genetics:
C;Comment: A common beta chain (CD18) forms a heterodimer with CD11b to form Mac-1 or

Query Match   63.8%;
Best Local Similarity   65.5%;   Score 3818; DB 1; Length 1163;
Conservative 138; Mismatches 253; Indels 6; Gaps 5;
Matches 755; Pred. No. 5.9e-267;

Qy   1 TFGTVLLLSVLASYHGFNLDVEEPTFQEDAGGFGQSVVQFGGSRLVVGAPLEVVAANQT 60

```
Db    1082  LPGQEAFMRAQTTTVLEKYKVHNPTLIVGSSIGGLLLLALITAVLYKVGFFKRQYKEKM 1141

Qy    1137  EDKPEDTATFSG 1148
            :||
Db    1142  EEANGQIAPENG 1153
```

RESULT 2

RHH01B
A;Reference number: 1
A;Accession: A31108
A;Molecule type: mRNA
A;Residues: 1-1153 <COR>
A;Cross-references: GB:J03925; NID:g187284; PIDN:AAA59544.-.; PID:g307148
A;Note: part of this sequence was confirmed by protein sequencing
R;Arnaout, M.A.; Gupta, S.K.; Pierce, M.W.; Tenen, D.G.
J;Cell Biol. 106, 2153-2158, 1988
A;Title: Amino acid sequence of the alpha subunit of human leukocyte adhesion recept
A;Reference number: A41600
A;Accession: A41600
A;Molecule type: DNA
A;Residues: 1-9 <SHE>
A;Cross-references: GB:M18044
R;Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 257-261, 1989
A;Title: cDNA sequence for the alphaM subunit of the human neutrophil adherence rece

Qy   4   TRAALLLFTALATSLGFNLDTEELTAPRVDSAGRGDSVVQYANSWVVVGAPQKITAANQT 63
            |||:::::|::|::||:.|: |||::|:::|.||:.::|:::|::::.||||.||||:: ||||

Qy   61   GRLYDCAAATGMCQPIPLHIRPEAVNMSLGLTLAASTNGSRLLACGPTLHRVCGENSYSK 120
            :||:||:||.|:.||::|::..|:||||||||||||||||||:||||:||||||||||| 63

Qy   121   GSCLLLGSRWEIIQTVPDATTPECPHQEMDIVFLIDGSGSIDQNDFNQMKGFVQAVMGQFE 180

Qy   181   GTDTLFALMQYSNLLKIHFTFTQFRTSPSQQSLVDPIVQLKGLTFTATGILTVTQLFHH 240

Qy   241   KNGARKSARKILIVITDGQKYKDPLEYSDVIPQAEKAGIIRYAIGVGHAFQGPTARQELN 300

Qy   301   TISSAPPQDHVFKVDNFAALGSIQKQLQEKIYAVEGTQSRASSSFQHEMSQEGFSTALTM 360

Qy   361   DGLFLGAVGSFSWSGGAFLYPPNMSPTFINMSQENVDMRDSYLGYSTELALWKGVQNLVL 420

Qy   421   GAPRYQHTGKAVIFTQVSRQWRKKAEVTGTQIGSYFGASLCSVDVDSDGSTDLILIGAPH 480

Qy   481   YYEQTRGGQVSVCPLPRGQRVQWQCDAVLRGEQGHPWGRFGAALTVLGDVNEDKLIDVAI 543

Qy   541   GAPGEQENRGAVYLFHGASEGISPSHSQRIASSQLSPRLQYFGQALSGGQDLTQDGLMD 600

Qy   601   LAVGARGQVLLRSLPVLKVGVAMRFSPVEVAKAVYRCWEEKPSALEAGDATVCLTIQKS 660

Qy   661   SLDQLG--DIQSSVRFDLALDPGRLTSRAIFNETKNPLTTRRKTLGLGIHCETLKLLLPD 718

Qy   722   CVEDSVTPITLRLNFTLVGKPLLAFRNLRPMLAADAQRYFTASLPFEKNGQADHICQ2NL 781

Qy   779   GVTLSFSGLQTLTVGSSLELNVIVTWNAGEDSYGTVVSLYPPAGLSHRRVSGAQKPHQ 838

Qy   782   GISFSSPGLKSLLVGSNLELNAEVMWNDGEDSYGTTITFSHPAGLSYRYVAEGQKQGQL 841

Qy   839   SALRLACETVPTEDEGLRSSRCSVNHPIFHEGSNGTFIVTFDVSYKATLGDRMLMRASAS 898

Qy   899   SENNKASSSKATFCLELPVKYAVYTMISRQEESTKYFNFATDEKKMKEAEHRYRVNNLS 958

Qy   902   SENNTPRTSKTTFCQLELPVKYAVTTVVSSHEQFTKYLNFSESESEKESHVAMRYQVNNLG 961

Qy   959   QRDLAISINFWVPVLLNGVAVW-DVVMEAP-SQSLPCVSERKPQHSDFLTQISRSPMLD 1016

Qy   962   QRDLPVSINFWVPVELNGEAVWMDVEVSHPQNPSLRCSSEKIAPPASDFLAHIQKNPVLD 1021

Qy   1017 CSIADCLQPRCDVPSFSVQEELDFTLKGNLSFGWVRETLQKKVLVVSVAEIIFDTSVYSQ 1076

Qy   1022 CSIAGCLRFRCDVPSFSVQEELDFTLKGNLSFGWVRQILQKKVSVSVAEIIFDTSVYSQ 1081

Qy   1077 LPGQEAFMRAQMEMVLEEDEVVNAIPIIMGSSVGALLLALITATLYKLGFFKRHYKEML 1136
```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:     August 26, 2003, 10:24:48 ; Search time 29 Seconds
            (without alignments)
            1882.690 Million cell updates/sec

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Title:          US-09-891-943-2
Perfect score:  5987
Sequence:       1 TFGTVLLLSVLASYHGFNLD..........DTATFSGDDFSCVAPNVPLS 1161

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters:     127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | % Query Match | Length | Match DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 5987 | 100.0 | 1162 | 1 | Q13349 | ITAD_HUMAN | homo sapien |
| 2 | 3815 | 63.7 | 1163 | 1 | P20702 | ITAX_HUMAN | homo sapien |
| 3 | 3439 | 57.4 | 1152 | 1 | P11215 | ITAM_HUMAN | homo sapien |
| 4 | 3327.5 | 55.6 | 1153 | 1 | P05555 | ITAM_MOUSE | mus musculu |
| 5 | 1476 | 24.7 | 1170 | 1 | P20701 | ITAL_HUMAN | homo sapien |
| 6 | 1457.5 | 24.3 | 1163 | 1 | P24063 | ITAL_MOUSE | mus musculu |
| 7 | 1156.5 | 19.3 | 1167 | 1 | Q60677 | ITAE_MOUSE | mus musculu |
| 8 | 1148 | 19.2 | 1179 | 1 | P38570 | ITAE_HUMAN | homo sapien |
| 9 | 1146.5 | 19.1 | 1189 | 1 | Q9UKX5 | ITAH_HUMAN | homo sapien |
| 10 | 1131.5 | 18.9 | 1167 | 1 | O75578 | ITAG_HUMAN | homo sapien |
| 11 | 1030.5 | 17.2 | 1151 | 1 | P56199 | ITA1_HUMAN | homo sapien |
| 12 | 1030 | 17.2 | 1180 | 1 | P18614 | ITA1_RAT | rattus norv |
| 13 | 1012 | 16.9 | 1178 | 1 | Q62469 | ITA2_MOUSE | mus musculu |
| 14 | 1007.5 | 16.8 | 1170 | 1 | P53712 | ITA2_BOVIN | bos taurus |
| 15 | 1007.5 | 16.8 | 1181 | 1 | P53710 | ITA2_HUMAN | homo sapien |
| 16 | 654.5 | 10.9 | 1038 | 1 | P17301 | ITA2_HUMAN | homo sapien |
| 17 | 646.5 | 10.8 | 1039 | 1 | P13612 | ITA4_HUMAN | homo sapien |
| 18 | 585.5 | 9.8 | 1032 | 1 | O00651 | ITA4_MOUSE | mus musculu |
| 19 | 584.5 | 9.8 | 1035 | 1 | Q91687 | ITA4_XENLA | xenopus lae |
| 20 | 579.5 | 9.7 | 1053 | 1 | Q13797 | ITA9_HUMAN | homo sapien |
| 21 | 570.5 | 9.5 | 1066 | 1 | Q62470 | ITA3_MOUSE | mus musculu |
| 22 | 554 | 9.3 | 1049 | 1 | P17852 | ITA3_CRISP | cricetidae |
| 23 | 547 | 9.1 | 1039 | 1 | P08648 | ITA5_HUMAN | homo sapien |
| 24 | 540.5 | 9.0 | 1049 | 1 | P08514 | ITA8_HUMAN | homo sapien |
| 25 | 538 | 9.0 | 1066 | 1 | P26006 | ITA3_HUMAN | homo sapien |
| 26 | 535.5 | 9.0 | 1033 | 1 | Q9qum0 | ITA8_MOUSE | mus musculu |
| 27 | 534 | 8.9 | 1053 | 1 | P11688 | ITA5_MOUSE | mus musculu |
| 28 | 534 | 8.9 | 1034 | 1 | Q06074 | ITAV_CHICK | gallus gall |
| 29 | 525.5 | 8.8 | 1050 | 1 | P26008 | ITA5_XENLA | xenopus lae |
| 30 | 497 | 8.3 | 1044 | 1 | P12080 | ITAV_DROME | drosophila |
| 31 | 496.5 | 8.3 | 1072 | 1 | P43406 | ITAV_MOUSE | mus musculu |
| 32 | 493 | 8.3 | 1048 | 1 | P26007 | ITA6_CHICK | gallus gall |
| 33 | 490 | 8.2 | 1146 | 1 | P06756 | ITA1_DROME | drosophila |
| 34 | 486 | 8.1 | 1130 | 1 | P23229 | ITA6_HUMAN | homo sapien |
| 35 | 482.5 | 8.1 | 1025 | 1 | P53708 | ITA8_HUMAN | homo sapien |
| 36 | 477.5 | 8.0 | 1044 | 1 | P26009 | ITA8_CHICK | gallus gall |
| 37 | 455 | 7.6 | 1181 | 1 | Q13683 | ITA7_HUMAN | homo sapien |
| 38 | 437.5 | 7.3 | 1091 | 1 | Q61739 | ITA6_MOUSE | mus musculu |
| 39 | 431.5 | 7.2 | 1226 | 1 | P34446 | PAT2_CAEEL | caenorhabdi |
| 40 | 430.5 | 7.2 | 1179 | 1 | Q61738 | ITA7_MOUSE | mus musculu |
| 41 | 429.5 | 7.2 | 1115 | 1 | O44396 | ITA3_DROME | drosophila |
| 42 | 420.5 | 7.0 | 1106 | 1 | Q63258 | ITA5_DROME | rattus norv |
| 43 | 411.5 | 6.9 | 1000 | 1 | Q9wlm8 | ITA7_DROME | drosophila |
| 44 | 408.5 | 6.8 | 1015 | 1 | Q9v7a4 | ITA4_DROME | drosophila |
| 45 | 394 | 6.6 | 1139 | 1 | Q03600 | INA1_CAEEL | caenorhabdi |

## ALIGNMENTS

RESULT 1
ITAD_HUMAN

ID   ITAD_HUMAN     STANDARD;     PRT;   1162 AA.
AC   Q13349; Q15575; Q15576;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Integrin alpha-D precursor (Leukointegrin alpha D) (CD11d) (ADB2).
GN   ITGAD.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=96111956; PubMed=8777714;
RA   Van der Vieren M., Le Trong H., Wood C.L., Moore P.F., St John T.,
RA   Staunton D.E., Gallatin W.M.;
RT   "A novel leukointegrin, alpha d beta 2, binds preferentially to ICAM-
RT   3.";
RL   Immunity 3:683-690(1995).
RN   [2]
RP   SEQUENCE OF 1-235 FROM N.A.
RX   MEDLINE=20187620; PubMed=10727744;
RA   Noti J.D., Johnson A.K., Dillon J.D.;
RT   "Structural and functional characterization of the leukocyte integrin
RT   gene CD11d. Essential role of Sp1 and Sp3.";
RL   J. Biol. Chem. 275:8959-8969(2000).
RN   [3]
RP   SEQUENCE OF 467-537, 571-602, 633-666; 788-834 AND 910-1125 FROM N.A.
RX   MEDLINE=96257236; PubMed=8666289;
RA   Wong D.A., Davis E.M., LeBeau M., Springer T.A.;
RT   "Cloning and chromosomal localization of a novel gene-encoding a human
RT   beta 2-integrin alpha subunit.";
RL   Gene 171:291-294(1996).
RN   [4]
RP   INTERACTION WITH VCAM1.
RX   MEDLINE=99059842; PubMed=9841932;
RA   Grayson M.H., Van der Vieren M., Sterbinsky S.A., Michael Gallatin W.,
RA   Hoffman P.A., Staunton D.E., Bochner B.S.;
RT   "alphadbeta2 integrin is expressed on human eosinophils and functions
RT   as an alternative ligand for vascular cell adhesion molecule 1
RT   (VCAM-1).";
RL   J. Exp. Med. 188:2187-2191(1998).
RN   [5]
RP   INTERACTION WITH VCAM1.
RX   MEDLINE=99370002; PubMed=10438935;
RA   Van der Vieren M., Crowe D.T., Hoekstra D., Vazeux R., Hoffman P.A.,
RA   Grayson M.H., Bochner B.S., Gallatin W.M., Staunton D.E.;
RT   "The leukocyte integrin alpha D beta 2 binds VCAM-1: evidence for a
RT   binding interface between I domain and VCAM-1.";
RL   J. Immunol. 163:1984-1990(1999).
CC   -!- FUNCTION: INTEGRIN ALPHA-D/BETA-2 IS A RECEPTOR FOR ICAM3 AND
CC       VCAM1. MAY PLAY A ROLE IN THE ATHEROSCLEROTIC PROCESS SUCH AS
CC       CLEARING LIPOPROTEINS FROM PLAQUES AND IN PHAGOCYTOSIS OF BLOOD-

```
CC       BORNE PATHOGENS, PARTICULATE MATTER, AND SENESCENT ERYTHROCYTES
CC       FROM THE BLOOD.
CC   -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-D
CC       ASSOCIATES WITH BETA-2.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: EXPRESSED MODERATELY ON MYELOMONOCYTIC CELL
CC       LINES AND SUBSETS OF PERIPHERAL BLOOD LEUKOCYTES AND STRONGLY ON
CC       TISSUE-SPECIALIZED CELLS, INCLUDING MACROPHAGES FOAM CELLS WITHIN
CC       ATHEROSCLEROTIC PLAQUES, AND ON SPLENIC RED PULP MACROPHAGES.
CC   -!- DOMAIN: THE INTEGRIN I-DOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS
CC       WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.
CC   -!- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.
CC   -!- SIMILARITY: Contains 1 VWFA domain.
CC   -!- SIMILARITY: Contains 7 FG-GAP repeats.
CC   --------------------------------------------------------------------------
```

```
DR   EMBL; U37028; AAB38547.1; -.
DR   EMBL; U40274; AAB60634.1; -.
DR   EMBL; U40275; AAB60635.1; -.
DR   EMBL; U40276; AAB60636.1; -.
DR   EMBL; U40277; AAB60637.1; -.
DR   EMBL; U40278; AAB60638.1; -.
DR   EMBL; U40279; AAB60638.1; JOINED.
DR   EMBL; AF187881; AAF62875.1; -.
DR   HSSP; P11215; 1A8X.
DR   Genew; HGNC:6146; ITGAD.
DR   MIM; 602453; -.
DR   GO; GO:0008305; C:integrin complex; TAS.
DR   GO; GO:0004895; F:cell adhesion receptor activity; TAS.
DR   GO; GO:0016337; P:cell-cell adhesion; NAS.
DR   GO; GO:0007160; P:cell-matrix adhesion; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR000413; Integrin_alpha.
DR   InterPro; IPR002035; VWF_A.
DR   Pfam; PF01839; FG-GAP; 3.
DR   Pfam; PF00357; integrin_A; 1.
DR   Pfam; PF00092; vwa; 1.
DR   PRINTS; PR01185; INTEGRINA.
DR   PRINTS; PR00453; VWFADOMAIN.
DR   SMART; SM00191; Int_alpha; 4.
DR   SMART; SM00327; VWA; 1.
DR   PROSITE; PS00242; INTEGRIN_ALPHA; 1.
DR   PROSITE; PS50234; VWFA; 1.
KW   Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
KW   Signal; Repeat; Calcium;
KW   Magnesium.
FT   SIGNAL        1     17
FT   CHAIN        18   1162       INTEGRIN ALPHA-D.
FT   DOMAIN       18   1100       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   1101   1124       POTENTIAL.
FT   DOMAIN     1125   1162       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       32     85       FG-GAP 1.
FT   REPEAT        ?      ?       FG-GAP 2.
FT   DOMAIN      150    332       VWFA.
FT   REPEAT      350    400       FG-GAP 3.
FT   REPEAT      401    452       FG-GAP 4.
FT   REPEAT      454    516       FG-GAP 5.
FT   REPEAT      518    576       FG-GAP 6.
FT   REPEAT      581    633       FG-GAP 7.
FT   CA_BIND     465    473       POTENTIAL.
FT   CA_BIND     530    538       POTENTIAL.
FT   CA_BIND     593    601       POTENTIAL.
FT   SITE       1127   1131       GFFKR MOTIF.
FT   DISULFID     67     74       BY SIMILARITY.
FT   DISULFID    106    124       BY SIMILARITY.
FT   DISULFID    655    710       BY SIMILARITY.
FT   DISULFID    769    775       BY SIMILARITY.
FT   DISULFID    846    861       BY SIMILARITY.
FT   DISULFID    994   1018       BY SIMILARITY.
FT   DISULFID   1023   1028       BY SIMILARITY.
FT   CARBOHYD     59     59       N-LINKED (GLCNAC). (POTENTIAL).
FT   CARBOHYD     87     87       N-LINKED (GLCNAC). (POTENTIAL).
FT   CARBOHYD     99     99       N-LINKED (GLCNAC). (POTENTIAL).
FT   CARBOHYD    391    391       N-LINKED (GLCNAC). (POTENTIAL).
FT   CARBOHYD    691    691       N-LINKED (GLCNAC). (POTENTIAL).
FT   CARBOHYD    733    733       N-LINKED (GLCNAC). (POTENTIAL).
FT   CARBOHYD    873    873       N-LINKED (GLCNAC). (POTENTIAL).
FT   CARBOHYD    957    957       N-LINKED (GLCNAC). (POTENTIAL).
FT   CARBOHYD   1046   1046       N-LINKED (GLCNAC). (POTENTIAL).
FT   CONFLICT    500    500       MISSING (IN REF. 2).
FT   CONFLICT    515    518       GHPW -> ATP (IN REF. 2).
FT   CONFLICT    525    525       L -> V (IN REF. 2).
FT   CONFLICT    984    984       V -> A (IN REF. 2).
SQ   SEQUENCE   1162 AA;  126885 MW;  F296A1A3454SD77D CRC64;
```

```
Query Match                100.0%;     Score 5987;   DB 1;   Length 1162;
Best Local Similarity      100.0%;     Pred. No. 0;
Matches 1161;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy    1 TFGTVLLLSVLASYHGFRLDVEEPTIFQEDAGGFGQGQSVVQFGGSRLVVGAPLEVVAANQT 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2 TFGTVLLLSVLASYHGFRLDVEEPTIFQEDAGGFGQGQSVVQFGGSRLVVGAPLEVVAANQT 61

Qy   61 GRLYDCAAATGMCQPIPLHIRPEAVNMSLGLTLAASTNGSRLLACGPTLHRVCGENSYSK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   62 GRLYDCAAATGMCQPIPLHIRPEAVNMSLGLTLAASTNGSRLLACGPTLHRVCGENSYSK 121

Qy  121 GSCLLLGSRWEIIQTVPDATPECPHQEMDIVFLIDGSGSIDQNDFNQMKGFVQAVMGQFE 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db  122 GSCLLLGSRWEIIQTVPDATPECPHQEMDIVFLIDGSGSIDQNDFNQMKGFVQAVXGQFE 181

Qy  181 GTDTLFALMQYSNLLKIHFTFTQFRTSPSQQSLVDPIVQLKGLTFTARGILTVVTQLFHH 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  182 GTDTLFALMQYSNLLKIHFTFTQFRTSPSQQSLVDPIVQLKGLTFTARGILTVVTQLFHH 241

Qy  241 KNGARKSAKKILIVITDGQKYKDPLEYSDVIPQAEKAGIIRYAIGVGHAFQGPTARQELN 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  242 KNGARKSAKKILIVITDGQKYKDPLEYSDVIPQAEKAGIIRYAIGVGHAFQGPTARQELN 301

Qy  301 TISSAPPQDHVFKVDNFAALGSIQKQLQEKIYAVEVGTQSRASSSFQHEMSQEGFSTALTM 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  302 TISSAPPQDHVFKVDNFAALGSIQKQLQEKIYAVEVGTQSRASSSFQHEMSQEGFSTALTM 361

Qy  361 DGLFLGAVSSFPSWSGGAFLYPPNMSPTFINMSQENVDMRDSYLGYSTELALWKGVQNLVL 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  362 DGLFLGAVSSFPSWSGGAFLYPPNMSPTFINMSQENVDMRDSYLGYSTELALWKGVQNLVL 421

Qy  421 GAPRYQHTGKAVIFTQVSRQWRKKAEVTGTQIGSYFGASLCSVDVDSDGSTDLILLIGAPH 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  422 GAPRYQHTGKAVIFTQVSRQWRKKAEVTGTQIGSYFGASLCSVDVDSDGSTDLILLIGAPH 481

Qy  481 YYEQTRGGQVSVCFLPRGCRVQWQCDAVLRGEQGHPWGRFGAALTVLGDVNEDKLIDVAI 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  482 YYEQTRGGQVSVCFLPRGCRVQWQCDAVLRGEQGHPWGRFGAALTVLGDVNEDKLIDVAI 541

Qy  541 GAPGEQENRGAVYLFHGASESGISPSHSQRIASSQLSPRLQYFGQALSGGQDLTQDGLMD 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  542 GAPGEQENRGAVYLFHGASESGISPSHSQRIASSQLSPRLQYFGQALSGGQDLTQDGLMD 601

Qy  601 LAVGARGQVLLLRSLPVLKVGVAMRFSPVEVAKAVYRCWEEKPSALEAGDATVCLTIQKS 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  602 LAVGARGQVLLLRSLPVLKVGVAMRFSPVEVAKAVYRCWEEKPSALEAGDATVCLTIQKS 661

Qy  661 SLDQLGDIQSSVRFDLALDPGRLTSRAIFNETKNPTLTRRKTLGLGIHCETLKLLLPDCV 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  662 SLDQLGDIQSSVRFDLALDPGRLTSRAIFNETKNPTLTRRKTLGLGIHCETLKLLLPDCV 721

Qy  721 EDVVSPIILHLNFSLVREPIPSPQNLRPVLAVSSQQLFTASLPFRKNCGQDGLCEGDLGV 780
```

OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: August 26, 2003, 10:24:28 ; Search time 91 Seconds
                 (without alignments)
                 2025.072 Million cell updates/sec

Title: US-09-891-943-2
Perfect score: 5987
Sequence: 1 TFGTVLLLSVLASYHGFNLD..........DTATFSGDDFSCVAPNVPLS 1161

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5
Searched: 1107863 seqs, 15872573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_19Jun03:*
                 1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
                 2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
                 3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
                 4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
                 5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
                 6: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
                 7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
                 8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
                 9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
                 10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
                 11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
                 12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
                 13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
                 14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
                 15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
                 16: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
                 17: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
                 18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
                 19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
                 20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
                 21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
                 22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
                 23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
                 24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5987	100.0	1161	16	AAR78166	Human beta-2 integ
2	5987	100.0	1161	18	AAW23049	Human beta 2 integ
3	5987	100.0	1161	19	AAW72825	Human alpha-d. Ho
4	5987	100.0	1161	19	AAW57491	Human beta2 integr
5	5987	100.0	1161	21	AAB07359	Human alpha_d clon
6	5987	100.0	1161	23	ABG61468	Human Beta2 integr
7	5981	99.9	1161	19	AAW65089	Human Beta-integri
8	5981	99.9	1161	20	AAW73342	Human alphad prote
9	5971.5	99.7	1161	18	AAW23064	Human beta 2 integ

ALIGNMENTS

RESULT 1
AAR78166

ID   AAR78166 standard; Protein; 1161 AA.
XX
AC   AAR78166;
XX
DT   28-DEC-1995 (first entry)
XX
DE   Human beta-2 integrin alpha-d.
XX
KW   Beta-2 integrin alpha-d subunit; antiinflammatory;
KW   inflammatory bowel disease; asthma.
XX
OS   Homo sapiens.
XX

	Key	Location/Qualifiers
FH		
FT	Domain	17..1108
FT		/note= "extracellular domain"
FT	Region	150..352
FT		/note= "this region is homologous to the insert
FT		common to CD11a,b,c and may be a site for
FT		interaction with ICAM family proteins"
FT	Binding-site	465..474
FT		/note= "putative cation binding site"
FT	Binding-site	518..527
FT		/note= "putative cation binding site"
FT	Binding-site	592..600
FT		/note= "putative cation binding site"
FT	Region	1109..1128
FT		/note= "transmembrane region"
FT	Domain	1129..1161
FT		/note= "cytoplasmic domain"

10	5971.5	99.7	1161	19	AAW72837	Human alpha-d deri
11	5971.5	99.7	1161	20	AAW65106	Human Beta-integri
12	5971.5	99.7	1161	20	AAW73343	Human alphad prote
13	5971.5	99.7	1161	21	AAB07376	Human alpha_d prot
14	5971.5	99.7	1161	23	ABG61485	Human Beta2_integr
15	4403.5	73.6	1161	18	AAW23062	Rat beta 2 integri
16	4403.5	73.6	1161	19	AAW72824	Rat alpha-d #1. R
17	4403.5	73.6	1161	19	AAW65004	Rat alpha d polype
18	4403.5	73.6	1161	21	AAW07374	Rat alpha d protei
19	4403.5	73.6	1161	23	ABG61483	Rat Beta2_integrin
20	4397.5	73.5	1161	20	AAW65104	Rat beta-integrin
21	4397.5	73.5	1161	20	AAW73345	Rat alphad protein
22	4395.5	73.4	1161	16	AAW73169	Rat alpha-d subuni
23	4365.5	72.9	1161	18	AAR78179	Rat beta 2 compos
24	4364.5	72.9	1161	18	AAW23059	Rat beta 2 integri
25	4364.5	72.9	1161	19	AAW72834	Rat alpha-d #2. R
26	4364.5	72.9	1161	19	AAW65101	Rat alpha-d polype
27	4364.5	72.9	1161	20	AAW60001	Rat alphad protein
28	4364.5	72.9	1161	20	AAW73344	Rat alpha d polype
29	4364.5	72.9	1161	21	AAB07371	Rat alpha d partia
30	4364.5	72.9	1151	23	ABG61480	Rat Beta2_integrin
31	4305.5	71.9	1161	18	AAW23061	Mouse beta 2 integ
32	4305.5	71.9	1161	19	AAW72836	Mouse alpha-d #2.
33	4305.5	71.9	1161	19	AAW65103	Mouse alpha-d poly
34	4305.5	71.9	1161	20	AAW60003	Mouse alphad prote
35	4305.5	71.9	1161	21	AAW73347	Mouse alphad prote
36	4305.5	71.9	1161	23	ABG61482	Mouse Beta2_integr
37	4303.5	71.9	1161	16	AAR78168	Mouse alpha-d subu
38	4303.5	71.9	1155	16	AAR78167	Mouse alpha-d subu
39	4278.5	71.5	1155	16	AAW73060	Mouse beta 2 integ
40	4278.5	71.5	1155	18	AAW23060	Mouse beta 2 integ
41	4278.5	71.5	1155	19	AAW72835	Mouse alpha-d #1.
42	4278.5	71.5	1155	19	AAW65102	Mouse alpha-d poly
43	4278.5	71.5	1155	20	AAW60002	Mouse alpha d poly
44	4278.5	71.5	1155	20	AAW73346	Mouse alphad prote
45	4278.5	71.5	1155	21	AAW07372	Mouse alpha d prot

```
XX
PN   WO9517412-A1.
XX
PD   29-JUN-1995.
XX
PF   21-DEC-1994;     94WO-US14832.
XX
PR   05-AUG-1994;     94US-0288689.
PR   23-DEC-1993;     93US-0173497.
XX
PA   (ICOS-) ICOS CORP.
XX
PI   Gallatin WM, Van Der Vieren M;
XX
DR   WPI; 1995-240603/31.
DR   N-PSDB; AAQ91712.
XX
PT   Alpha sub-unit polypeptide of human beta 2 integrin - used to
PT   identify potential antiinflammatory agents, for the treatment of
PT   graft arteriosclerosis, inflammatory bowel disease, asthma, etc.
XX
PS   Claim 7; Page 82-87; 172pp; English.
XX
CC   A probe based on a partial cDNA clone (given in AAQ91727) of canine
CC   alpha-TM1 was used to screen a human spleen cDNA library to identify
CC   clone 19A2 encoding the beta-1 integrin alpha-subunit, alpha-d.
CC   The cDNA was manipulated to allow expression of recombinant alpha-d
CC   subunit in COS and CHO cells.
XX
SQ   Sequence   1161 AA;

Query Match             100.0%;  Score 5997;  DB 16;  Length 1161;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 1161;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy          1 TFGTVLLLSVLASYHGFNLDVEEPTIFQEDAGGFGQSVVQFGGSRLVVGAPLEVVAANQT 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TFGTVLLLSVLASYHGFNLDVEEPTIFQEDAGGFGQSVVQFGGSRLVVGAPLEVVAANQT 60

Qy         61 GRLYDCAAATGMCQPIPLHIRPEAVNMSLGLTLAASTNGSRLLACGPTLHRVCGENSYSK 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GRLYDCAAATGMCQPIPLHIRPEAVNMSLGLTLAASTNGSRLLACGPTLHRVCGENSYSK 120

Qy        121 GSCLLLGSRWEIIQTVPDATPECPHQEMDIVFLIDGSGSIDQNDFNQMKGFVQAVMGQFE 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GSCLLLGSRWEIIQTVPDATPECPHQEMDIVFLIDGSGSIDQNDFNQMKGFVQAVMGQFE 180

Qy        181 GTDTLFALMQYSNLLKIHFTFTQFRTRSPSQQSLVDPIVQLKGLTFTATGILTTVVTQLFH 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTDTLFALMQYSNLLKIHFTFTQFRTRSPSQQSLVDPIVQLKGLTFTATGILTTVVTQLFH 240

Qy        241 KNGARKSAKKILILIVITDGQKYKDPLEYSDVIFQAEKAGIIRYAIGVGHAFQGPTARQELN 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 KNGARKSAKKILILIVITDGQKYKDPLEYSDVIFQAEKAGIIRYAIGVGHAFQGPTARQELN 300

Qy        301 TISSAPPQDHVFKVDNFAALGSIQKQLQEKIYAVEGTQSRASSSFQHEMSQEGFSTALTM 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TISSAPPQDHVFKVDNFAALGSIQKQLQEKIYAVEGTQSRASSSFQHEMSQEGFSTALTM 360

Qy        361 DGLFLGAVGSFSWSGGAFLYPPNMSPTFINMSQENVDMRDSYLGYSTELALMKGVQNLVL 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DGLFLGAVGSFSWSGGAFLYPPNMSPTFINMSQENVDMRDSYLGYSTELALMKGVQNLVL 420

Qy        421 GAPRYQHTGKAVIFTQVSRQWRKKAEVTGTQIGSYFGASLCSVDVDSDGSTDLILIGAPH 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GAPRYQHTGKAVIFTQVSRQWRKKAEVTGTQIGSYFGASLCSVDVDSDGSTDLILIGAPH 480

Qy        481 YYEQTRGGQVSVCPLPRGQRVQWQCDAVLRGEQGHPWGRFGAALTVLGDVNEDKLIDVAI 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 YYEQTRGGQVSVCPLPRGQRVQWQCDAVLRGEQGHPWGRFGAALTVLGDVNEDKLIDVAI 540

Qy        541 GAPGEQENRGAVYLFHGASESGISPSHSQRIASSQLSPRLQYFGQALSGGQDLTQCGLMD 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAPGEQENRGAVYLFHGASESGISPSHSQRIASSQLSPRLQYFGQALSGGQDLTQCGLMD 600

Qy        601 LAVGARGQVLLLRSLPVLKVGVAMRFSPVEVAKAVYRCWEEKPSALEAGDATVCLTIQKS 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LAVGARGQVLLLRSLPVLKVGVAMRFSPVEVAKAVYRCWEEKPSALEAGDATVCLTIQKS 660

Qy        661 SLDQLGDIQSSVRFDLALDPGRLTSRAIFNETKNPPLTTRKTLGLGIHCETLKLLLPDCV 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 SLDQLGDIQSSVRFDLALDPGRLTSRAIFNETKNPPLTTRKTLGLGIHCETLKLLLPDCV 720

Qy        721 EDVVSPIILHLNFSLVREPIPSPQNLRPVLAVGSQDLFTASLPFEKNCGQDGLCEGDLGV 780
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 EDVVSPIILHLNFSLVREPIPSPQNLRPVLAVGSQDLFTASLPFEKNCGQDGLCEGDLGV 780

Qy        781 TLSFSGLQTLTVGSSLELNVTVTVWNRAGEDSYGTVVSLYYPAGLSHRRVSGAQKQPHSA 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TLSFSGLQTLTVGSSLELNVTVTVWNRAGEDSYGTVVSLYYPAGLSHRRVSGAQKQPHSA 840

Qy        841 LRLACETVPTEDEGLRSSRCSVNHPIFHEGSNGTFIVTFDVSYKATLGDRMLMRASASSE 900
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 LRLACETVPTEDEGLRSSRCSVNHPIFHEGSNGTFIVTFDVSYKATLGDRMLMRASASSE 900

Qy        901 NNKASSSKATFQLELPVKYAVYTMISRQEESTKYFNFATSDEKKMKEAEHRYRVNNLSQR 960
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 NNKASSSKATFQLELPVKYAVYTMISRQEESTKYFNFATSDEKKMKEAEHRYRVNNLSQR 960

Qy        961 DLAISINFWVPVLLNGVAVWDVVMEARSQSLPCVSERKPPQHSDFLTQISRSSPMLDCSIA 1020
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 DLAISINFWVPVLLNGVAVWDVVMEARSQSLPCVSERKPPQHSDFLTQISRSSPMLDCSIA 1020

Qy       1021 DCLQFRCDVPSFSVQEELDFTLKGNLSFGWVRETLQKKVLVVSVAEITFDTSVYSQLPGQ 1080
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 DCLQFRCDVPSFSVQEELDFTLKGNLSFGWVRETLQKKVLVVSVAEITFDTSVYSQLPGQ 1080

Qy       1081 EAFMRAQMEMVLEEDSVYNAIPIIMGSSVGALLLLALITAVLYKLGFFKRHYKEMLEDKP 1140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 EAFMRAQMEMVLEEDSVYNAIPIIMGSSVGALLLLALITAVLYKLGFFKRHYKEMLEDKP 1140

Qy       1141 EDTATFSGDDFSCVAPNVPLS 1161
              |||||||||||||||||||||
Db       1141 EDTATFSGDDFSCVAPNVPLS 1161


RESULT 2
AAW23049
ID   AAW23049 standard; Protein; 1161 AA.
XX
AC   AAW23049;
XX
DT   24-FEB-1998  (first entry)
XX
DE   Human beta 2 integrin alpha d subunit.
XX
KW   Beta 2 integrin alpha d subunit; human; cell migration;
KW   cell adhesion; phagocytosis; diabetes; atherosclerosis;
KW   multiple sclerosis; asthma; psoriasis; lung inflammation;
KW   acute respiratory distress syndrome; rheumatoid arthritis.
OS   Homo sapiens.
XX
FH   Key              Location/Qualifiers
FT
FT   Domain           17..1108
FT                    /label= Extracellular_domain
FT   Domain           1109..1128
FT                    /label= Transmembrane_domain
FT                    /note= "homologous to the human CD11c transmembrane
FT                    region"
FT   Domain           1:29..1161
FT                    /label= Cytoplasmic_domain
FT   Domain           150..352
FT                    /note= "region homologous to the I (insertion)
FT                    domain common to CD11a, CD11b and CD11c"
XX
```

OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: August 26, 2003, 10:37:23 ; Search time 71 Seconds
2157.853 Million cell updates/sec
(without alignments)

Title: US-09-891-943-2
Perfect score: 5987
Sequence: 1 TFGTVLLLSVLASYHGFNLD..........DTATFSGDDFSCVAPNVPLS 1161

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 497079 seqs, 131961718 residues
Total number of hits satisfying chosen parameters: 497079

Post-processing: Minimum Match 0%
Maximum Match 100%
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database : Published Applications AA:*
Listing first 45 summaries

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a,
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5987	100.0	1161	9	US-09-350-259-2	Sequence 2, Appli
2	5987	100.0	1161	11	US-09-891-943-2	Sequence 2, Appli
3	5971.5	99.7	1161	9	US-09-350-259-99	Sequence 99, App
4	5971.5	99.7	1161	11	US-09-891-943-99	Sequence 99, App
5	4403.5	73.6	1161	11	US-09-350-259-55	Sequence 55, Appl
6	4403.5	73.6	1161	9	US-09-891-943-55	Sequence 55, Appl
7	4364.5	72.9	1151	9	US-09-350-259-37	Sequence 37, Appl
8	4364.5	72.9	1151	11	US-09-891-943-37	Sequence 37, Appl
9	4305.5	71.9	1151	9	US-09-350-259-53	Sequence 53, Appl
10	4305.5	71.9	1161	11	US-09-891-943-53	Sequence 53, Appl
11	4278.5	71.5	1155	9	US-09-350-259-46	Sequence 46, Appl
12	4278.5	71.5	1155	11	US-09-891-943-46	Sequence 46, Appl
13	3746	62.6	1163	9	US-09-350-259-4	Sequence 4, Appli
14	3746	62.6	1163	11	US-09-891-943-4	Sequence 4, Appli
15	3455	57.7	1153	9	US-09-350-259-3	Sequence 3, Appli

16	3455	57.7	1153	11	US-09-902-481A-1	Sequence 1, Appli
17	3455	57.7	1153	11	US-09-891-943-3	Sequence 3, Appli
18	3455	57.7	1153	15	US-10-144-259-30	Sequence 30, Appl
19	3455	57.7	1153	15	US-10-207-655-176	Sequence 176, App
20	3439.5	57.4	1152	10	US-09-945-265-4	Sequence 4, Appli
21	3417	57.1	1137	11	US-09-902-481A-6	Sequence 6, Appli
22	3411	57.0	1137	11	US-09-902-481A-5	Sequence 5, Appli
23	3401	56.8	1137	11	US-09-902-481A-4	Sequence 4, Appli
24	3388	56.6	1137	11	US-09-902-481A-3	Sequence 3, Appli
25	1833	30.6	494	9	US-09-350-259-103	Sequence 103, App
26	1833	30.6	494	11	US-09-891-943-103	Sequence 103, App
27	1531	25.6	413	9	US-09-350-259-101	Sequence 101, App
28	1531	25.6	413	11	US-09-891-943-101	Sequence 101, App
29	1476	24.7	413	10	US-09-945-265-2	Sequence 2, Appli
30	1148	19.2	1170	10	US-10-177-550-2	Sequence 2, Appli
31	1146.5	19.1	1179	12	US-10-177-550-2	Sequence 2, Appli
32	1146.5	19.1	1189	12	US-09-984-130-35	Sequence 35, Appl
33	1037.5	17.3	1034	11	US-09-836-353A-35	Sequence 35, Appl
34	1037.5	17.3	1034	12	US-09-984-130-43	Sequence 43, Appl
35	1030.5	17.2	1151	11	US-09-836-353A-43	Sequence 43, Appl
36	1030.5	17.2	1151	12	US-09-984-130-103	Sequence 103, App
37	1007.5	16.8	1181	11	US-09-836-353A-103	Sequence 103, App
38	979	16.4	191	11	US-09-160-354-2	Sequence 3, Appli
39	979	16.4	191	11	US-10-160-354-2	Sequence 3, Appli
40	873.5	14.6	191	11	US-09-805-354-3	Sequence 3, Appli
41	873.5	14.6	707	9	US-10-144-259-3	Sequence 3, Appli
42	840.5	14.0	264	15	US-10-125-540-313	Sequence 313, App
43	840.5	14.0	264	15	US-09-764-870-313	Sequence 313, App
44	655.5	10.9	1038	11	US-09-350-259-93	Sequence 93, Appl
45	610.5	10.2	199	15	US-09-891-943-93	Sequence 93, Appl
				11	US-10-207-655-127	Sequence 127, App
				15	US-10-066-551-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-350-259-2

Sequence 2, Application US/09350259
Patent No. US20020062008A1
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: NO. US20020062008A1e1 Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/350,259
CURRENT FILING DATE: 1999-07-08
EARLIER APPLICATION NUMBER: 09/193,043
EARLIER FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1993-12-23
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 1161
TYPE: PRT
ORGANISM: Homo sapiens
US-09-350-259-2

Query Match   100.0%;   Score 5987;   DB 9;   Length 1161;
Best Local Similarity   100.0%;
Matches 1161;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 TFGTVLLLSVLASYHGFNLDVEEPIFIFQEDAGGFGQSVVQFGGSRLVVGAPLEVVAANQT 60
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 TFGTVLLLSVLASYHGFNLDVEEPIFIFQEDAGGFGQSVVQFGGSRLVVGAPLEVVAANQT 60

Qy   61 GRLYDCAAATGMCQPIPLHIRPEAVNMSLGLTLAASTNGSRLLACGPTLHRVCGENSYSK 120

Left alignment

```
Db    61 GRLYDCAAATGMCQPIPLHIRPEAVNMSLGITLAASTNGSRLLACGPTLHRVCGENSYSK  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   121 GSCLLLGSRWEIIQTVPDATPECPHQEMDIVFLIDGSGSIDQNDFNQMKGFVQAVMGQFE  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GSCLLLGSRWEIIQTVPDATPECPHQEMDIVFLIDGSGSIDQNDFNQMKGFVQAVMGQFE  180

Qy   181 GTDTLFALMQYSNLLKIHFTFTQFRTSPSQQSLVDPIVQLKGLTFTATGILTVVTQLFHH  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GTDTLFALMQYSNLLKIHFTFTQFRTSPSQQSLVDPIVQLKGLTFTATGILTVVTQLFHH  240

Qy   241 KNGARKSAKKILIVITDGQKYKDPLEYSDVIPQAEKAGIIRYAIGVGHAFQGPTARQELN  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 KNGARKSAKKILIVITDGQKYKDPLEYSDVIPQAEKAGIIRYAIGVGHAFQGPTARQELN  300

Qy   301 TISSAPPQDHVFKVDNFAALGSIQKQLQEKIYAVEGTQSRASSSFQHEMSQEGFSTALTM  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 TISSAPPQDHVFKVDNFAALGSIQKQLQEKIYAVEGTQSRASSSFQHEMSQEGFSTALTM  360

Qy   361 DGLFLGAVGSFSWSGGAFLYPPNMSPTFINMSQENVDMRDSYLGYSTELALMKGVQNLVL  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 DGLFLGAVGSFSWSGGAFLYPPNMSPTFINMSQENVDMRDSYLGYSTELALMKGVQNLVL  420

Qy   421 GAPRYQHTGKAVIFTQVSRQWRKKAEVTGTQIGSYFGASLCSVDVDSDGSTDLLIGAPH  480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GAPRYQHTGKAVIFTQVSRQWRKKAEVTGTQIGSYFGASLCSVDVDSDGSTDLLIGAPH  480

Qy   481 YYEQTRGGQVSVCPLPRGQRVQWQCDAVLRGEQGHPWGRFGAALTVLGDVNEDKLIDVAI  540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 YYEQTRGGQVSVCPLPRGQRVQWQCDAVLRGEQGHPWGRFGAALTVLGDVNEDKLIDVAI  540

Qy   541 GAPGEQENRGAVYLFHGASESGISPSHSQRIASSQLSPRLQYFGQALSGGQDLTQDGLMD  600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GAPGEQENRGAVYLFHGASESGISPSHSQRIASSQLSPRLQYFGQALSGGQDLTQDGLMD  600

Qy   601 LAVGARGQVLLRSLPVLKVGVAMRFSPVEVAKAVYRCWEEKPSALEAGDATVCLTIQKS  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 LAVGARGQVLLRSLPVLKVGVAMRFSPVEVAKAVYRCWEEKPSALEAGDATVCLTIQKS  660

Qy   661 SLDQLGDIQSSVRFDLALDPGRLTSRAIFNETKNPTLTRRKTLGLGIHCETLKLLLPDCV  720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 SLDQLGDIQSSVRFDLALDPGRLTSRAIFNETKNPTLTRRKTLGLGIHCETLKLLLPDCV  720

Qy   721 EDVVSPIILHLNFSLVREPIPSPQNLRPVLAVGSQDLFTASLPFEKNCGQDGLCEGDLGV  780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 EDVVSPIILHLNFSLVREPIPSPQNLRPVLAVGSQDLFTASLPFEKNCGQDGLCEGDLGV  780

Qy   781 TLSFSGLQTLTVGSSLELNVIVTVWNAGEDSYGTVVSLYYPAGLSHRRVSGAQKQPHQSA  840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TLSFSGLQTLTVGSSLELNVIVTVWNAGEDSYGTVVSLYYPAGLSHRRVSGAQKQPHQSA  840

Qy   841 LRLACETVPTEDEGLRSSRCSVNHPIFHEGSNGTFIVTFDVSYKATLGDRMLMRASASSE  900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 LRLACETVPTEDEGLRSSRCSVNHPIFHEGSNGTFIVTFDVSYKATLGDRMLMRASASSE  900

Qy   901 NNKASSSKRATFQLELPVKYAVYTMISRQEESTKYFNFATSTDSEKKMKEAEHRYRVNNLSQR  960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 NNKASSSKRATFQLELPVKYAVYTMISRQEESTKYFNFATSTDSEKKMKEAEHRYRVNNLSQR  960

Qy   961 DLAISINFWVPVLLNGVAVWDVVMEAPSQSLPCVSERKPPQHSDFLTQISRSPMLDCSIA 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 DLAISINFWVPVLLNGVAVWDVVMEAPSQSLPCVSERKPPQHSDFLTQISRSPMLDCSIA 1020

Qy  1021 DCLQFRCDVPSFSVQEELDFTLKGNLSFGWVRETLQKVLVVSVAEITFDTSVYSQLPGQ 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 DCLQFRCDVPSFSVQEELDFTLKGNLSFGWVRETLQKVLVVSVAEITFDTSVYSQLPGQ 1080

Qy  1081 EAFMRAQMEMVLEEDEVVNAIPIIMGSSVGALLLLALITATLYKLGFFKRHYKEMLEDKP 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 EAFMRAQMEMVLEEDEVVNAIPIIMGSSVGALLLLALITATLYKLGFFKRHYKEMLEDKP 1140

Qy  1141 EDTATFSGDDFSCVAPNVPLS 1161
         |||||||||||||||||||||
```

```
Db  1141 EDTATFSGDDFSCVAPNVPLS 1161
```

RESULT 2

US-09-891-943-2

Sequence 2, Application US/09891943

Publication No. US20030072728A1

GENERAL INFORMATION:
  APPLICANT: Gallatin, Michael W.
  APPLICANT: Van der Vieren, Monica
  TITLE OF INVENTION: No. US20030072728A1el Human 2
  FILE REFERENCE: 27806/35004
  CURRENT APPLICATION NUMBER: US/09/891,943
  CURRENT FILING DATE: 2001-06-26
  PRIOR APPLICATION NUMBER: 09/193,043
  PRIOR FILING DATE: 1998-11-16
  PRIOR APPLICATION NUMBER: 08/286,889
  PRIOR FILING DATE: 1994-08-05
  PRIOR APPLICATION NUMBER: 08/362,652
  PRIOR FILING DATE: 1994-12-21
  PRIOR APPLICATION NUMBER: 08/943,363
  PRIOR FILING DATE: 1997-10-03
  NUMBER OF SEQ ID NOS: 114
  SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2
  TYPE: PRT
  LENGTH: 1161
  ORGANISM: Homo sapiens
US-09-891-943-2

Query Match   100.0%;   Score 5987;   DB 11;   Length 1161;
Best Local Similarity 100.0%;   Pred. No. 0;   Indels 0;
Matches 1161;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Right alignment

```
Qy     1 TFGTVLLLSVLLASYHGFNLDVEEPTIFQEDDAGGFGQQSVVQFGGSRLIVVGAPLEVVVAANQT  60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 TFGTVLLLSVLLASYHGFNLDVEEPTIFQEDDAGGFGQQSVVQFGGSRLIVVGAPLEVVAANQT  60

Qy    61 GRLYDCAAATGMCQPIPLHIRPEAVNMSLGITLAASTNGSRLLACGPTLHRVCGENSYSK  120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GRLYDCAAATGMCQPIPLHIRPEAVNMSLGITLAASTNGSRLLACGPTLHRVCGENSYSK  120

Qy   121 GSCLLLGSRWEIIQTVPDATPECPHQEMDIVFLIDGSGSIDQNDFNQMKGFVQAVMGQFE  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GSCLLLGSRWEIIQTVPDATPECPHQEMDIVFLIDGSGSIDQNDFNQMKGFVQAVMGQFE  180

Qy   181 GTDTLFALMQYSNLLKIHFTFTQFRTSPSQQSLVDPIVQLKGLTFTATGILTVVTQLFHH  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GTDTLFALMQYSNLLKIHFTFTQFRTSPSQQSLVDPIVQLKGLTFTATGILTVVTQLFHH  240

Qy   241 KNGARKSAKKILIVITDGQKYKDPLEYSDVIPQAEKAGIIRYAIGVGHAFQGPTARQELN  300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 KNGARKSAKKILIVITDGQKYKDPLEYSDVIPQAEKAGIIRYAIGVGHAFQGPTARQELN  300

Qy   301 TISSAPPQDHVFKVDNFAALGSIQKQLQEKIYAVEGTQSRASSSFQHEMSQEGFSTALTM  360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 TISSAPPQDHVFKVDNFAALGSIQKQLQEKIYAVEGTQSRASSSFQHEMSQEGFSTALTM  360

Qy   361 DGLFLGAVGSFSWSGGAFLYPPNMSPTFINMSQENVDMRDSYLGYSTELALMKGVQNLVL  420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 DGLFLGAVGSFSWSGGAFLYPPNMSPTFINMSQENVDMRDSYLGYSTELALMKGVQNLVL  420

Qy   421 GAPRYQHTGKAVIFTQVSRQWRKKAEVTGTQIGSYFGASLCSVDVDSDGSTDLLIGAPH  480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GAPRYQHTGKAVIFTQVSRQWRKKAEVTGTQIGSYFGASLCSVDVDSDGSTDLLIGAPH  480

Qy   481 YYEQTRGGQVSVCPLPRGQRVQWQCDAVLRGEQGHPWGRFGAALTVLGDVNEDKLIDVAI  540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 YYEQTRGGQVSVCPLPRGQRVQWQCDAVLRGEQGHPWGRFGAALTVLGDVNEDKLIDVAI  540

Qy   541 GAPGEQENRGAVYLFHGASESGISPSHSQRIASSQLSPRLQYFGQALSGGQDLTQDGLMD  600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GAPGEQENRGAVYLFHGASESGISPSHSQRIASSQLSPRLQYFGQALSGGQDLTQDGLMD  600
```

OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: August 26, 2003, 10:32:48 ; Search time 32 seconds
(without alignments)
1535.091 Million cell updates/sec

Title:
Perfect score: 5987
Sequence: 1 TFGTVLLLSVLASYHGFNLD.........DTATFSGDDFSCVAPNVPLS 1161

Scoring table:
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5987	100.0	1161	3	US-09-193-043-2	Sequence 2, Appl
2	5987	100.0	1161	4	US-09-688-307A-4	Sequence 2, Appl
3	5981	99.9	1161	1	US-08-173-497-2	Sequence 2, Appli
4	5981	99.9	1161	1	US-08-286-889-2	Sequence 2, Appli
5	5981	99.9	1161	1	US-08-485-618-2	Sequence 2, Appli
6	5981	99.9	1161	1	US-08-362-652-2	Sequence 2, Appli
7	5981	99.9	1161	2	US-08-605-672-2	Sequence 2, Appli
8	5981	99.9	1161	2	US-08-482-293A-2	Sequence 2, Appli
9	5981	99.9	1161	2	US-08-943-363-2	Sequence 2, Appli
10	5971.5	99.7	1161	1	US-08-485-618-99	Sequence 99, Appl
11	5971.5	99.7	1161	1	US-08-605-672-99	Sequence 99, Appl
12	5971.5	99.7	1161	1	US-08-482-293A-99	Sequence 99, Appl
13	5971.5	99.7	1161	2	US-08-943-363-99	Sequence 99, Appl
14	5971.5	99.7	1161	2	US-08-193-043-99	Sequence 99, Appl
15	5971.5	99.7	1161	4	US-09-688-307A-99	Sequence 99, Appl
16	4403.5	73.6	1161	3	US-09-193-043-55	Sequence 55, Appl
17	4403.5	73.6	1161	4	US-09-688-307A-55	Sequence 55, Appl
18	4397.5	73.5	1161	2	US-08-482-293A-55	Sequence 55, Appl
19	4397.5	73.5	1161	1	US-08-362-652-55	Sequence 55, Appl
20	4397.5	73.5	1161	1	US-08-605-672-55	Sequence 55, Appl
21	4397.5	73.5	1161	2	US-08-482-293A-55	Sequence 55, Appl
22	4397.5	73.5	1161	2	US-08-943-363-55	Sequence 55, Appl
23	4364.5	72.9	1161	1	US-08-286-889-37	Sequence 37, Appl
24	4364.5	72.9	1151	1	US-08-485-618-37	Sequence 37, Appl
25	4364.5	72.9	1151	1	US-08-362-652-37	Sequence 37, Appl
26	4364.5	72.9	1151	2	US-08-605-672-37	Sequence 37, Appl
27	4364.5	72.9	1151	2	US-08-482-293A-37	Sequence 37, Appl
28	4364.5	72.9	1151	2	US-08-943-363-37	Sequence 37, Appl
29	4364.5	72.9	1151	3	US-09-193-043-37	Sequence 37, Appl
30	4364.5	72.9	1151	4	US-09-688-307A-37	Sequence 37, Appl
31	4305.5	71.9	1161	1	US-08-485-618-53	Sequence 53, Appl
32	4305.5	71.9	1161	1	US-08-362-652-53	Sequence 53, Appl
33	4305.5	71.9	1161	2	US-08-605-672-53	Sequence 53, Appl
34	4305.5	71.9	1161	2	US-08-482-293A-53	Sequence 53, Appl
35	4305.5	71.9	1161	2	US-08-943-363-53	Sequence 53, Appl
36	4305.5	71.9	1161	3	US-09-193-043-53	Sequence 53, Appl
37	4305.5	71.9	1161	4	US-09-688-307A-53	Sequence 53, Appl
38	4278.5	71.5	1155	1	US-08-286-889-46	Sequence 46, Appl
39	4278.5	71.5	1155	1	US-08-485-618-46	Sequence 46, Appl
40	4278.5	71.5	1155	1	US-08-362-652-46	Sequence 46, Appl
41	4278.5	71.5	1155	2	US-08-605-672-46	Sequence 46, Appl
42	4278.5	71.5	1155	2	US-08-482-293A-46	Sequence 46, Appl
43	4278.5	71.5	1155	2	US-08-943-363-46	Sequence 46, Appl
44	4278.5	71.5	1155	3	US-09-193-043-46	Sequence 46, Appl
45	4278.5	71.5	1155	4	US-09-688-307A-46	Sequence 46, Appl

ALIGNMENTS

RESULT 1
US-09-193-043-2

Sequence 2, Application US/09193043
Patent No. 6251395
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6251395el Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/193,043
CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1993-12-23
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 1161
TYPE: PRT
ORGANISM: Homo sapiens
US-09-193-043-2

Query Match 100.0%; Score 5987; DB 3; Length 1161;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFGTVLLLSVLASYHGFNLDVEEPIIFQEBAGGFGGSVVQFGGSRLVVGGAPLEVVAANQT 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 TFGTVLLLSVLASYHGFNLDVEEPIIFQEBAGGFGGSVVQFGGSRLVVGGAPLEVVAANQT 60

Qy 61 GRLYDCAAATGMCQPIPLHIRPEAVNMSLGUTLAASTNGSRLLACGPTLHRVCGENSYSK 120
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 GRLYDCAAATGMCQPIPLHIRPEAVNMSLGUTLAASTNGSRLLACGPTLHRVCGENSYSK 120

Qy 121 GSCLLLGSRWEIIQTVPDATPECPHQEMDIVFLIDGSGSIDQNDFNQMKGFVQAVMGQFE 180
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 GSCLLLGSRWEIIQTVPDATPECPHQEMDIVFLIDGSGSIDQNDFNQMKGFVQAVMGQFE 180

Qy 181 GTDTLFALMQYSNLLKIHFPTQQFRTSPSQQSLVDPIVQLKGLTFTATGILTVVTQLFHH 240
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 GTDTLFALMQYSNLLKIHFPTQQFRTSPSQQSLVDPIVQLKGLTFTATGILTVVTQLFHH 240

Qy 241 KNGARKSAKKILIVITDGQKYKDPLEYSDVIPQAEKAGIIRYAIGVGHAFQGGPTARQELN 300
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 KNGARKSAKKILIVITDGQKYKDPLEYSDVIPQAEKAGIIRYAIGVGHAFQGGPTARQELN 300

```
;  PRIOR APPLICATION NUMBER: 09/193,043
;  PRIOR FILING DATE: 1998-11-16
;  PRIOR APPLICATION NUMBER: 08/605,672
;  PRIOR FILING DATE: 1996-02-22
;  PRIOR APPLICATION NUMBER: 08/173,497
;  PRIOR FILING DATE: 1993-12-23
;  PRIOR APPLICATION NUMBER: 08/286,889
;  PRIOR FILING DATE: 1994-08-05
;  PRIOR APPLICATION NUMBER: 08/362,652
;  PRIOR FILING DATE: 1994-12-21
;  PRIOR APPLICATION NUMBER: 08/943,363
;  PRIOR FILING DATE: 1997-10-03
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: Patentin Ver. 2.0
;
US-09-688-307A-2
;
;  SEQ ID NO 2
;  LENGTH: 1161
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-688-307A-2

Query Match             100.0%;  Score 5987;  DB 4;  Length 1161;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 1161;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
```

Qy   1 TFGTVLLLSVLASYHGFNLDVEEPTIFQEDAGGEGQSVVQFGGSRLVVGAPLEVVAANQT 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 TFGTVLLLSVLASYHGFNLDVEEPTIFQEDAGGEGQSVVQFGGSRLVVGAPLEVVAANQT 60

Qy   61 GRLYDCAAATGMCQPIFLHIRPEAVNMSLGLTLAASTNGSRLLACGPTLHRVCGENSYSK 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GRLYDCAAATGMCQPIFLHIRPEAVNMSLGLTLAASTNGSRLLACGPTLHRVCGENSYSK 120